

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:58:31 ; Search time 15.3602 Seconds  
(without alignments)  
10767.297 Million cell updates/sec

Title: US-10-541-346-2

Perfect score: 20

Sequence: 1 ttgaatatattacaaagc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	95.0	715	4	US-09-925-065A-502888
C 2	19	95.0	819	5	US-10-027-632-166247
C 3	19	95.0	819	6	US-10-027-632-166247
4	18.4	92.0	607	4	US-09-925-065A-661036
5	18.4	92.0	647	4	US-09-925-065A-665667
C 6	18.4	92.0	8553	7	US-10-613-053A-1
C 7	18.4	92.0	8553	7	US-10-451-366A-1
8	18.4	92.0	180216	3	US-09-835-232-6
9	18.4	92.0	180216	6	US-10-308-485-6
10	18.4	92.0	271990	6	US-10-195-144-87
11	18.4	92.0	271990	6	US-10-345-072-87
C 12	18	90.0	372	4	US-09-925-065A-199410
C 13	18	90.0	372	4	US-09-925-065A-199411
14	18	90.0	844	5	US-10-027-632-155478
15	18	90.0	844	6	US-10-027-632-155478
C 16	18	90.0	4320	7	US-10-630-518-17
17	18	90.0	4320	7	US-10-630-518-21
C 18	17.4	87.0	546	4	US-09-925-065A-97366
C 19	17.4	87.0	562	4	US-09-925-065A-853310
C 20	17.4	87.0	596	4	US-09-925-065A-601207
C 21	17.4	87.0	596	4	US-09-925-065A-601208
22	17.4	87.0	226215	5	US-10-087-192-1948
23	16.8	84.0	211	4	US-09-925-065A-192206

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24 16.8 84.0 211 4 US-09-925-065A-192207 Sequence 192207,
c 25 16.8 84.0 214 9 US-10-926-683-63 Sequence 63, Appl
c 26 16.8 84.0 352 4 US-09-925-065A-371009 Sequence 371009,
c 27 16.8 84.0 368 4 US-09-925-065A-580465 Sequence 580465,
28 16.8 84.0 417 4 US-09-925-065A-642312 Sequence 642312,
29 16.8 84.0 417 4 US-09-925-065A-642314 Sequence 642314,
30 16.8 84.0 417 4 US-09-925-065A-642315 Sequence 642315,
31 16.8 84.0 417 4 US-09-925-065A-642316 Sequence 642316,
32 16.8 84.0 458 4 US-09-925-065A-747766 Sequence 747766,
33 16.8 84.0 468 5 US-10-027-632-92083 Sequence 92083, A
34 16.8 84.0 468 5 US-10-027-632-317894 Sequence 317894, A
35 16.8 84.0 468 6 US-10-027-632-92083 Sequence 92083, A
36 16.8 84.0 468 6 US-10-027-632-317894 Sequence 317894,
c 37 16.8 84.0 476 4 US-09-925-065A-797645 Sequence 797645,
38 16.8 84.0 478 7 US-10-242-535A-38621 Sequence 38621, A
c 40 16.8 84.0 478 7 US-10-085-783A-38621 Sequence 38621, A
41 16.8 84.0 502 4 US-09-925-065A-635386 Sequence 635386,
42 16.8 84.0 502 4 US-09-925-065A-222608 Sequence 222608,
43 16.8 84.0 507 4 US-09-925-065A-203071 Sequence 203071,
44 16.8 84.0 507 4 US-09-925-065A-585834 Sequence 585834,
45 16.8 84.0 535 4 US-09-925-065A-149328 Sequence 149328,

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#### ALIGNMENTS

RESULT 1  
US-09-925-065A-502888/c  
; Sequence 502888, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925.065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 502888  
; LENGTH: 715  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-502888

Query Match 95.0%; Score 19; DB 4; Length 715;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGAATATATATTACAAAG 19  
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Db 441 TTGAATATATATTACAAAG 423

RESULT 2  
US-10-027-632-166247/c  
; Sequence 166247, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 166247  
LENGTH: 819  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-166247

Query Match 95.0%; Score 19; DB 5; Length 819;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAG 19  
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Db 441 TTGAATATATATTACAAAG 423

RESULT 3  
US-10-027-632-166247/c  
Sequence 166247, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 166247  
LENGTH: 819  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-166247

Query Match 95.0%; Score 19; DB 6; Length 819;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAG 19  
|||||

Db 441 TTGAATATATATTACAAAG 423

RESULT 4  
US-09-925-065A-661036  
Sequence 661036, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 661036  
LENGTH: 607  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-661036

Query Match 92.0%; Score 18.4; DB 4; Length 607;  
Best Local Similarity 95.0%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20  
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Db 383 TTGAATATATATTACAAAGC 402

RESULT 5  
US-09-925-065A-665667  
Sequence 665667, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 665667  
LENGTH: 647  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-665667

Query Match 92.0%; Score 18.4; DB 4; Length 647;  
Best Local Similarity 95.0%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20  
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Db 317 TTGAAATATATATTACAAAGC 336

RESULT 6  
US-10-613-053A-1/c  
; Sequence 1, Application US/10613053A  
; Publication No. US20040088749A1  
; GENERAL INFORMATION:  
; APPLICANT: IMAMURA, Jun  
; APPLICANT: YANAGIDATE, Ritsuko  
; APPLICANT: SAKAI, Takako  
; APPLICANT: FUJIMOTO, Hideya  
; APPLICANT: KOIZUKA, Nobuya  
; APPLICANT: HAYAKAWA, Takahiko  
; TITLE OF INVENTION: A Protein Which is Involved in Recovery of Cytoplasm Male  
; TITLE OF INVENTION: Fertility from Sterility and a Gene Encoding the Protein  
; FILE REFERENCE: P23889  
; CURRENT APPLICATION NUMBER: US/10/613.053A  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR FILING DATE: PCT JP02/04092  
; PRIOR FILING DATE: 2002-04-24  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 8553  
; TYPE: DNA  
; ORGANISM: Raphanus sativus  
US-10-613-053A-1

Query Match 92.0%; Score 18.4; DB 7; Length 8553;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20  
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Db 4150 TTGAATATATATTACAAAGC 4131

RESULT 7  
US-10-451-366A-1/c  
; Sequence 1, Application US/10451366A  
; Publication No. US20040117868A1  
; GENERAL INFORMATION:  
; APPLICANT: IMAMURA, Jun  
; APPLICANT: YANAGIDATE, Ritsuko  
; APPLICANT: SAKAI, Takako  
; APPLICANT: FUJIMOTO, Hideya  
; APPLICANT: KOIZUKA, Nobuya  
; APPLICANT: HAYAKAWA, Takahiko  
; TITLE OF INVENTION: A Protein Which is Involved in Recovery of Cytoplasm Male  
; TITLE OF INVENTION: Fertility from Sterility and a Gene Encoding the Protein  
; FILE REFERENCE: P23888  
; CURRENT APPLICATION NUMBER: US/10/451.366A  
; CURRENT FILING DATE: 2003-12-23  
; PRIOR FILING DATE: PCT JP02/04092  
; PRIOR FILING DATE: 2002-04-24  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 8553  
; TYPE: DNA  
; ORGANISM: Raphanus sativus  
US-10-451-366A-1

Query Match 92.0%; Score 18.4; DB 7; Length 8553;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20  
|||||

Db 4150 TTGAATATATATTACAAAGC 4131

RESULT 8  
US-09-835-232-6  
; Sequence 6, Application US/09835232  
; Patent No. US20020098489A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leader, Benjamin  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/09/835,232  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 180216  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(180216)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-835-232-6

Query Match 92.0%; Score 18.4; DB 3; Length 180216;  
Best Local Similarity 95.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20  
|||||  
Db 56172 TTGAAATATATATTACAAAGC 56191

RESULT 9  
US-10-308-485-6  
; Sequence 6, Application US/10308485  
; Publication No. US20030170683A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leader, Benjamin  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/10/308,485  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: US/09/835,232  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 180216  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(180216)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-308-485-6

Query Match 92.0%; Score 18.4; DB 6; Length 180216;  
Best Local Similarity 95.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20  
|||||  
Db 56172 TTGAAATATATATTACAAAGC 56191

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RESULT 10
US-10-195-144-87
; Sequence 87, Application US/10195144
; Publication No. US20030126646A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; FILE REFERENCE: 16313-0136
; CURRENT APPLICATION NUMBER: US/10/195,144
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 271990
; TYPE: DNA
; ORGANISM: Raphanus sativum
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (144241)..(144300)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-195-144-87

Query Match          92.0%; Score 18.4; DB 6; Length 271990;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
Db 170571 TTGAATATATATTACAAAGC 170590

RESULT 11
US-10-345-072-87
; Sequence 87, Application US/10345072
; Publication No. US20030237112A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; APPLICANT: LAI, FANG MING
; APPLICANT: LEFOREST, MARTIN
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; FILE REFERENCE: 16313-0210
; CURRENT APPLICATION NUMBER: US/10/345,072
; PRIOR APPLICATION NUMBER: PCT/US02/22217
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.1
US-10-345-072-87

Query Match          92.0%; Score 18.4; DB 6; Length 271990;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
Db 170571 TTGAATATATATTACAAAGC 170590

RESULT 12
US-09-925-065A-199410/c
; Sequence 199410, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199410
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199410

Query Match          90.0%; Score 18; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAATATATATTACAAAGC 20
Db 205 GAATATATATTACAAAGC 188

RESULT 13
US-09-925-065A-199411/c
; Sequence 199411, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199411
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199411

Query Match          90.0%; Score 18; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188
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RESULT 14
US-10-027-632-155478
; Sequence 155478, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155478
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-155478

Query Match          90.0%; Score 18; DB 5; Length 844;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGAATATATATTACAAA 18
Db      827 TTGAATATATATTACAAA 844
|||||

RESULT 15
US-10-027-632-155478
; Sequence 155478, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
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; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155478
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-155478

Query Match          90.0%; Score 18; DB 6; Length 844;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGAATATATATTACAAA 18
Db      827 TTGAATATATATTACAAA 844
|||||

Search completed: March 31, 2006, 07:57:48
Job time : 17.3602 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 07:14:39 ; Search time 11.0903 Seconds  
(without alignments)  
7200.876 Million cell updates/sec

Title: US-10-541-346-2

Perfect score: 20

Sequence: 1 ttgaatatattacaaagc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

1: /SID55/ptodata/2/pubpna/US08 NEW PUB.seq.\*  
2: /SID55/ptodata/2/pubpna/US06 NEW PUB.seq.\*  
3: /SID55/ptodata/2/pubpna/US07 NEW PUB.seq.\*  
4: /SID55/ptodata/2/pubpna/PCT NEW PUB.seq.\*  
5: /SID55/ptodata/2/pubpna/US03 NEW PUB.seq.\*  
6: /SID55/ptodata/2/pubpna/US09 NEW PUB.seq.\*  
7: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq.\*  
8: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq.\*  
9: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq.\*  
10: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq.\*  
11: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq.\*  
12: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq.\*  
13: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq.\*  
14: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq.\*  
15: /SID55/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-10-541-346-2	Sequence 2, Appli
2	20	100.0	1675	US-10-541-346-4	Sequence 4, Appli
C 3	19	95.0	715	US-09-925-065A-502888	Sequence 502888,
4	18.4	92.0	607	US-09-925-065A-661036	Sequence 661036,
5	18.4	92.0	647	US-09-925-065A-665667	Sequence 665667,
C 6	18.4	92.0	789	US-10-301-480-607861	Sequence 607861,
C 7	18.4	92.0	789	US-10-301-480-1221270	Sequence 1221270,
C 8	18	90.0	369	US-10-301-480-288106	Sequence 288106,
C 9	18	90.0	369	US-10-301-480-288107	Sequence 288107,
C 10	18	90.0	369	US-10-301-480-901515	Sequence 901515,
C 11	18	90.0	369	US-10-301-480-901516	Sequence 901516,
C 12	18	90.0	372	US-09-925-065A-199410	Sequence 199410,
C 13	18	90.0	372	US-09-925-065A-199411	Sequence 199411,
C 14	17.4	87.0	546	US-09-925-065A-97366	Sequence 97366, A
C 15	17.4	87.0	553	US-10-301-480-198305	Sequence 198305,
C 16	17.4	87.0	553	US-10-301-480-811714	Sequence 811714,
C 17	17.4	87.0	562	US-09-925-065A-853310	Sequence 853310,
18	17.4	87.0	595	US-10-301-480-552100	Sequence 552100,

#### ALIGNMENTS

##### RESULT 1

US-10-541-346-2

; Sequence 2, Application US/10541346

; Publication No. US20060059590A1

; GENERAL INFORMATION:

; APPLICANT: Cerney, Eric

; APPLICANT: Duong, Can

; APPLICANT: Hart, Jesse

; APPLICANT: Huber, Scott

; APPLICANT: Krieb, Rachel

; APPLICANT: Listello, Jennifer

; APPLICANT: Martens, Amy

; APPLICANT: Sammons, Bernard

; TITLE OF INVENTION: Cotton Event MON 88913 and Compositions and Methods for Detection

; TITLE OF INVENTION: Thereof

; FILE REFERENCE: 11899.0239.PCUS00

; CURRENT APPLICATION NUMBER: US/10/541,346

; CURRENT FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: 60/447,184

; PRIOR FILING DATE: 2003-02-12

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chimeric DNA of cotton genomic DNA and transgene insert DNA

US-10-541-346-2

Query Match 100.0%; Score 20; DB 10; Length 20;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATTACAAAGC 20

Db 1 TTGAATATATTACAAAGC 20

##### RESULT 2

US-10-541-346-4

Sequence 1165509,  
Sequence 601207,  
Sequence 601208,  
Sequence 39609, A  
Sequence 39609, A  
Sequence 6745, Ap  
Sequence 2649, Ap  
Sequence 60916, A  
Sequence 60916, A  
Sequence 60916, A  
Sequence 20, Appl  
Sequence 89, Appl  
Sequence 192206,  
Sequence 192207,  
Sequence 281767,  
Sequence 895176,  
Sequence 281768,  
Sequence 895177,  
Sequence 441022,  
Sequence 1054431,  
Sequence 371009,  
Sequence 580465,  
Sequence 642312,  
Sequence 642314,  
Sequence 642315,  
Sequence 642316,  
Sequence 747766,  
Sequence 797645,



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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288106
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-288106

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GAATATATATTACAAAGC 20
        |||||
Db      205 GAATATATATTACAAAGC 188

RESULT 9
US-10-301-480-288107/c
; Sequence 288107, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288107
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-288107

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GAATATATATTACAAAGC 20
        |||||
Db      205 GAATATATATTACAAAGC 188

RESULT 10
US-10-301-480-901515/c
; Sequence 901515, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 901515
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-901515

Query Match          92.0%; Score 18.4; DB 10; Length 789;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGAATATATATTACAAAGC 20
        |||||
Db      51 TTGAATATATATTACAAAGC 32

RESULT 7
US-10-301-480-1221270/c
; Sequence 1221270, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1221270
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1221270

Query Match          92.0%; Score 18.4; DB 10; Length 789;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTGAATATATATTACAAAGC 20
        |||||
Db      51 TTGAATATATATTACAAAGC 32

RESULT 8
US-10-301-480-288106/c
; Sequence 288106, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288106
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-288106

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GAATATATATTACAAAGC 20
        |||||
Db      205 GAATATATATTACAAAGC 188

```

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; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901515
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-901515

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 11
US-10-301-480-901516/c
; Sequence 901516, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901516
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-901516

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 12
US-09-925-065A-199410/c
; Sequence 199410, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199410
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199410

Query Match          90.0%; Score 18; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 13
US-09-925-065A-199411/c
; Sequence 199411, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199411
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199411

Query Match          90.0%; Score 18; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 14
US-09-925-065A-97366/c
; Sequence 97366, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 957086
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; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 97366  
 ; LENGTH: 546  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-925-065A-97366

Query Match 87.0%; Score 17.4; DB 6; Length 546;  
 Best Local Similarity 94.7%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAATATATATTACAAAGC 20  
 |||||  
 Db 157 TGAATATATATTAAAAAGC 139

RESULT 15  
 US-10-301-480-198305/c  
 ; Sequence 198305, Application US/10301480  
 ; Publication No. US20060057564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
 ; FILE REFERENCE: 108827.137  
 ; CURRENT APPLICATION NUMBER: US/10/301,480  
 ; CURRENT FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 10/215,598  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/311,695  
 ; PRIOR FILING DATE: 2001-08-10  
 ; NUMBER OF SEQ ID NOS: 1226818  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 198305  
 ; LENGTH: 553  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-301-480-198305

Query Match 87.0%; Score 17.4; DB 9; Length 553;  
 Best Local Similarity 94.7%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAATATATATTACAAAGC 20  
 |||||  
 Db 164 TGAATATATATTAAAAAGC 146

Search completed: March 31, 2006, 07:57:17  
 Job time : 11.0903 secs







Db	241	GGTGAGAAATTGTTAGCGCACCTTACCAAAAGCATCTTTGCCTTTATTGCAAAAGATAAAG	300
Qy	2535	CAGATTCCCTCTAGTACAAAGTGGGGAAACAAATAACGTGGAAAGAGCGTCTGTGACAGCC	2594
Db	301	CAGATTCCCTCTAGTACAAAGTGGGGAAACAAATAACGTGGAAAGAGCTGCTGTGACAGCC	360
Qy	2595	CACTCACCTAAATGCGGTATGACGAAACGAGTGACGACCAACAAAGAAATTTAGTGCTTGAGCTTCAG	2654
Db	361	CACTCACCTAAATGCGGTATGACGAAACGAGTGACGACCAACAAAGAAATTTAGTGCTTGAGCTTCAG	420
Qy	2655	GATTTAGCAGCATTTCCAGATTGGGTTTCAATCAACAGAGTGACGACCATATCACTTTATTTC	2714
Db	421	GATTTAGCAGCATTTCCAGATTGGGTTTCAATCAACAGAGTGACGACCATATCACTTTATTTC	480
Qy	2715	AAATTGGTATGCGCAAAACCAAGAGGAACCTCCCATCTCAAAAGTTTGTGAAGGAAGAAT	2774
Db	481	AAATTGGTATGCGCAAAACCAAGAGGAACCTCCCATCTCAAAAGTTTGTGAAGGAAGAAT	540
Qy	2775	TCGATATCAAGCTTGATATCGGAAGTTTCTCTTTGAGGAGGTTGCTCGTGAATGGGA	2834
Db	541	TCGATATCAAGCTTGATATCGGAAGTTTCTCTTTGAGGAGGTTGCTCGTGAATGGGA	600
Qy	2835	CACATATGGTTGTTATATAAACCATTTCATGTCATGAGATTTT	2880
Db	601	CACATATGGTTGTTATATAAACCATTTCATGTCATGAGATTTT	646

## RESULT 2

```

US-09-737-626A-28
; Sequence 28, Application US/09737626A
; Patent No. 6660911
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intron
US-09-737-626A-28

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Query Match	22.4%	Score 646;	DB 3;	Length 1695;
Best Local Similarity	100.0%;	Pred. No. 2.7e-132;		
Matches 646;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2235	AATTCTCAGTCCAAAGCCTCAACAAGGTACAGGGTCTCCAAACATTAGCCAAA	2234	
DB	1	AATTCTCAGTCCAAAGCCTCAACAAGGTACAGGGTCTCCAAACATTAGCCAAA	60	
QY	2295	AGCTACAGGAGATCAATGAGACTCTTCATCAAAGTAAACTACTGTTCCAGCACATGCA	2354	
DB	61	AGCTACAGGAGATCAATGAGAAATCTTCATCAAAGTAAACTACTGTTCCAGCACATGCA	120	
QY	2355	TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT	2414	
DB	121	TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT	180	
QY	2415	TTCAAAAGTAAATCTTGTCCAAACATCAGACAGAGCTGGCTCTGGGGACACAGACAAAAAGCAAT	2474	

Db	181	TTGAAAGTAACTCTTGTCACATCGAGCAGCTGCCTGTGTGGGGACCGACACAAAAGGAAT	240
Qy	2475	GGTGCAGAAATTGTTAGCGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAG	2534
Db	241	GGTGCAGAAATTGTTAGCGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAG	300
Qy	2535	CAGATTCTCTAGTACAGTGGGGAAACAAAATAACGTTGGAAAGAGCTGCTCTGACAGCC	2594
Db	301	CAGATTCTCTAGTACAGTGGGGAAACAAAATAACGTTGGAAAGAGCTGCTCTGACAGCC	360
Qy	2595	CACCTCACTAATGGTATGACGAACGAGTGACGACCAACAAAAGAAATTAGCTTCGAGCTCAG	2654
Db	361	CACCTCACTAATGGTATGACGAACGAGTGACGACCAACAAAAGAAATTAGCTTCGAGCTCAG	420
Qy	2655	GATTTAGCAGCAATTCAGATTGGGTTTCAATCAACAAAGGTACGAGCCATATCACTTTATTC	2714
Db	421	GATTTAGCAGCAATTCAGATTGGGTTTCAATCAACAAAGGTACGAGCCATATCACTTTATTC	480
Qy	2715	AAATTGGTATCGGCAAAACCAAGAGGAACCTCCATCTCTCAAAAGGTTTGTAAAGGAAGAT	2774
Db	481	AAATTGGTATCGGCAAAACCAAGAGGAACCTCCATCTCTCAAAAGGTTTGTAAAGGAAGAT	540
Qy	2775	TGGATATCAAGCTTGATATCGGAAGTTTCTCTCTTGAGGGGAGGTGCTCGTGGAAATGGGA	2834
Db	541	TGGATATCAAGCTTGATATCGGAAGTTTCTCTCTTGAGGGGAGGTGCTCGTGGAAATGGGA	600
Qy	2835	CACATATGGTGTATAATAAACCAATTCATTTGTCATGAGATTTT	2880
Db	601	CACATATGGTGTATAATAAACCAATTCATTTGTCATGAGATTTT	646

### RESULT 3

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US-10-427-169-28
; Sequence 28, Application US/10427169
; Patent No. 6919495
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6919495el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/427,169
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides +
US-10-427-169-28

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	Query Match	22.4%	Score 646;	DB 3;	Length 1695;	
	Best Local Similarity	100.0%;	Pred. No. 2.7e-132;			
	Matches 646;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	2235	AATTCTCAGTCCAAAGCCTCAA	CAGGTC	CAGGTC	CAGAGTCTCCAAACCATTAGCCAAA	2294
Db	1	AATTCTCAGTCCAAAGCCTCAA	CAGGTC	CAGGTC	CAGAGTCTCCAAACCATTAGCCAAA	60
Qy	2295	AGGTCACAGGAGATCAATGAAG	ATCTTT	CAATCAAAGTAAACT	ACTGTTTCACAGACATGCA	2354
Db	61	AGGTCACAGGAGATCAATGAAG	ATCTTT	CAATCAAAGTAAACT	ACTGTTTCACAGACATGCA	120
Qy	2355	TCATGGTCAGTAAGTTTT	CAGAAAAAGACATCC	CACCGAAGAC	TTTAAAGTTTAGTGGGCATCT	2414

Db 121 TCAATGTCAGTAAGTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180  
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Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAAGCAACAAAAGGAAT 240  
Qy 2475 GTGCGAGAATTGTAGGGCGCCTTACCAAAAGCATCTTTGCCCTTTATTGCGAAAGATAAG 2534  
Db 241 GTGCGAGAATTGTAGGGCGCCTTACCAAAAGCATCTTTGCCCTTTATTGCGAAAGATAAG 300  
Qy 2535 CAGATTCTCTAGTACAAGTGGGGACCAAAATAACCTGGGAAGAGCTGTCTGACAGCC 2594  
Db 301 CAGATTCTCTAGTACAAGTGGGGACCAAAATAACCTGGGAAGAGCTGTCTGACAGCC 360  
Qy 2595 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTTAGCTTGAGCTCAG 2654  
Db 361 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTTAGCTTGAGCTCAG 420  
Qy 2655 GATTTAGCAGATTCAGATTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTTATTC 2714  
Db 421 GATTTAGCAGATTCAGATTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTTATTC 480  
Qy 2715 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCTCCTCAAGGTTTGTAGGAAGAAT 2774  
Db 481 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCTCCTCAAGGTTTGTAGGAAGAAT 540  
Qy 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTCTCTGCGTAATGGGA 2834  
Db 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTCTCTGCGTAATGGGA 600  
Qy 2835 CACATATGGTTGTTATAATAAACCAATTCATTTGTCATGAGATTTT 2880  
Db 601 CACATATGGTTGTTATAATAAACCAATTCATTTGTCATGAGATTTT 646

## RESULT 4

US-10-427-180-28  
; Sequence 28, Application US/10427180  
; Patent No. 6949696  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen  
; APPLICANT: Flasiński, Stanislaw  
; APPLICANT: Wilkinson, Jack  
; TITLE OF INVENTION: No. 6949696el Plant Expression Constructs  
; FILE REFERENCE: 38-21(51499)B  
; CURRENT APPLICATION NUMBER: US/10/427,180  
; CURRENT FILING DATE: 2003-05-01  
; PRIOR APPLICATION NUMBER: US/09/737,626A  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 09/737,626  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 1695  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(1695)  
; OTHER INFORMATION: n = a or g or c or t/u, r = g or a, y = t/u or c  
; OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intro  
US-10-427-180-28

Query Match 22.4%; Score 646; DB 3; Length 1695;  
Best Local Similarity 100.0%; Pred. No. 2.7e-132;  
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2235 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294  
Db 1 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

Qy 2295 AGCTACAGAGATCAATGAAGAATCTTCAATCAAAGTAAATCTCTGTTCCAGCACATGCA 2354  
Db 61 AGCTACAGAGATCAATGAAGAATCTTCAATCAAAGTAAATCTCTGTTCCAGCACATGCA 120  
Qy 2355 TCATGTCAGTAAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414  
Db 121 TCATGTCAGTAAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180  
Qy 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAAGCAACAAAAGGAAT 2474  
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAAGCAACAAAAGGAAT 240  
Qy 2475 GTGCGAGAATTGTAGGGCGCCTTACCAAAAGCATCTTTGCCCTTTATTGCGAAAGATAAG 2534  
Db 241 GTGCGAGAATTGTAGGGCGCCTTACCAAAAGCATCTTTGCCCTTTATTGCGAAAGATAAG 300  
Qy 2535 CAGATTCTCTAGTACAAGTGGGGACCAAAATAACCTGGGAAGAGCTGTCTGACAGCC 2594  
Db 301 CAGATTCTCTAGTACAAGTGGGGACCAAAATAACCTGGGAAGAGCTGTCTGACAGCC 360  
Qy 2595 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTTAGCTTGAGCTCAG 2654  
Db 361 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTTAGCTTGAGCTCAG 420  
Qy 2655 GATTTAGCAGATTCAGATTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTTATTC 2714  
Db 421 GATTTAGCAGATTCAGATTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTTATTC 480  
Qy 2715 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCTCCTCAAGGTTTGTAGGAAGAAT 2774  
Db 481 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCTCCTCAAGGTTTGTAGGAAGAAT 540  
Qy 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTCTCTGCGTAATGGGA 2834  
Db 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTCTCTGCGTAATGGGA 600  
Qy 2835 CACATATGGTTGTTATAATAAACCAATTCATTTGTCATGAGATTTT 2880  
Db 601 CACATATGGTTGTTATAATAAACCAATTCATTTGTCATGAGATTTT 646

## RESULT 5

US-09-737-698B-27  
; Sequence 27, Application US/09737698B  
; Patent No. 6462258  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen  
; APPLICANT: Wilkinson, Jack  
; TITLE OF INVENTION: No. 6462258el Plant Expression Constructs  
; FILE REFERENCE: 38-21(51499)C  
; CURRENT APPLICATION NUMBER: US/09/737,698B  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/171,173  
; PRIOR FILING DATE: 1999-12-16  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 1946  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(1946)  
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides + Act11  
US-09-737-698B-27

Query Match 19.0%; Score 548; DB 3; Length 1946;  
Best Local Similarity 100.0%; Pred. No. 9.4e-111;  
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2235 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294  
Db 1 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 111

Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60  
QY 2295 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 2354  
Db 61 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 120  
QY 2355 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 2414  
Db 121 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 180  
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 2474  
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 240  
QY 2475 GGTGAGCAATTTGTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 2534  
Db 241 GGTGAGCAATTTGTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300  
QY 2535 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 2594  
Db 301 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 360  
QY 2595 CACTCACTAATGCGTATGACGAAACGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 2654  
Db 361 CACTCACTAATGCGTATGACGAAACGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 420  
QY 2655 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTTC 2714  
Db 421 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTTC 480  
QY 2715 AAATTTGGTATCGCCAAAACCAAGAGGAATCTCCATCTCTCAAAAGTTTGTGAAGGAAGAT 2774  
Db 481 AAATTTGGTATCGCCAAAACCAAGAGGAATCTCCATCTCTCAAAAGTTTGTGAAGGAAGAT 540  
QY 2775 TCGATATC 2782  
Db 541 TCGATATC 548

RESULT 6  
US-09-737-626A-27  
; Sequence 27, Application US/09737626A  
; Patent No. 6660911  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen  
; APPLICANT: Flaszinski, Stanislaw  
; APPLICANT: Wilkinson, Jack  
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs  
; FILE REFERENCE: 38-21(51499)B  
; CURRENT APPLICATION NUMBER: US/09/737,626A  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 09/737,626  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 1946  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(1946)  
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +  
; OTHER INFORMATION: ntro  
US-09-737-626A-27

Query Match 19.0%; Score 548; DB 3; Length 1946;  
Best Local Similarity 100.0%; Pred. No. 9.4e-111;  
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294  
Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

QY 2295 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 2354  
Db 61 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 120  
QY 2355 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 2414  
Db 121 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 180  
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 2474  
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 240  
QY 2475 GGTGAGCAATTTGTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 2534  
Db 241 GGTGAGCAATTTGTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300  
QY 2535 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 2594  
Db 301 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 360  
QY 2595 CACTCACTAATGCGTATGACGAAACGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 2654  
Db 361 CACTCACTAATGCGTATGACGAAACGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 420  
QY 2655 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTTC 2714  
Db 421 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTTC 480  
QY 2715 AAATTTGGTATCGCCAAAACCAAGAGGAATCTCCATCTCTCAAAAGTTTGTGAAGGAAGAT 2774  
Db 481 AAATTTGGTATCGCCAAAACCAAGAGGAATCTCCATCTCTCAAAAGTTTGTGAAGGAAGAT 540  
QY 2775 TCGATATC 2782  
Db 541 TCGATATC 548

## RESULT 7

US-10-427-169-27  
; Sequence 27, Application US/10427169  
; Patent No. 6919495  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen  
; APPLICANT: Flaszinski, Stanislaw  
; APPLICANT: Wilkinson, Jack  
; TITLE OF INVENTION: No. 6919495el Plant Expression Constructs  
; FILE REFERENCE: 38-21(51499)B  
; CURRENT APPLICATION NUMBER: US/10/427,169  
; CURRENT FILING DATE: 2003-05-01  
; PRIOR APPLICATION NUMBER: US/09/737,626A  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 09/737,626  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 1946  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(1946)  
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +  
; OTHER INFORMATION: ntro  
US-10-427-169-27

Query Match 19.0%; Score 548; DB 3; Length 1946;  
Best Local Similarity 100.0%; Pred. No. 9.4e-111;  
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294  
Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTGAGGTGACAGAGTCTCCAAACCATTTAGCCAAA 60  
QY 2295 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAACTACTGTTCCAGCACATGCA 2354  
Db 61 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAACTACTGTTCCAGCACATGCA 120  
QY 2355 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 2414  
Db 121 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 180  
QY 2415 TTGAAGTAACTCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACACAGACAAAAAAGGAAT 2474  
Db 181 TTGAAGTAACTCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACACAGACAAAAAAGGAAT 240  
QY 2475 GGTGCAAGATTTGTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 2534  
Db 241 GGTGCAAGATTTGTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 300  
QY 2535 CAGATTCCTCTAGTACAAAGTGGGGACAAATAAAGTGGAAAGAGCTGCTCCAGACGCC 2594  
Db 301 CAGATTCCTCTAGTACAAAGTGGGGACAAATAAAGTGGAAAGAGCTGCTCCAGACGCC 360  
QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAAAAGAAATTTAGCTTCGAGCTCAG 2654  
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAAAAGAAATTTAGCTTCGAGCTCAG 420  
QY 2655 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714  
Db 421 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480  
QY 2715 AAATTTGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 2774  
Db 481 AAATTTGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 540  
QY 2775 TCGATATC 2782  
Db 541 TCGATATC 548

RESULT 8  
US-10-427-180-27  
; Sequence 27, Application US/10427180  
; Patent No. 6949696  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen  
; APPLICANT: Flasiński, Stanislaw  
; APPLICANT: Wilkinson, Jack  
; TITLE OF INVENTION: No. 6949696el Plant Expression Constructs  
; FILE REFERENCE: 38-21(51499)B  
; CURRENT APPLICATION NUMBER: US/10/427,180  
; CURRENT FILING DATE: 2003-05-01  
; PRIOR APPLICATION NUMBER: US/09/737,626A  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 09/737,626  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 1946  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(1946)  
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides + Act11  
; OTHER INFORMATION: ntro  
US-10-427-180-27

Query Match 19.0%; Score 548; DB 3; Length 1946;  
Best Local Similarity 100.0%; Pred. No. 9.4e-111;  
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTGAGGTGACAGAGTCTCCAAACCATTTAGCCAAA 2294

Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTGAGGTGACAGAGTCTCCAAACCATTTAGCCAAA 60  
QY 2295 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAACTACTGTTCCAGCACATGCA 2354  
Db 61 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAACTACTGTTCCAGCACATGCA 120  
QY 2355 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 2414  
Db 121 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 180  
QY 2415 TTGAAGTAACTCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACACAGACAAAAAAGGAAT 2474  
Db 181 TTGAAGTAACTCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACACAGACAAAAAAGGAAT 240  
QY 2475 GGTGCAAGATTTGTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 2534  
Db 241 GGTGCAAGATTTGTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 300  
QY 2535 CAGATTCCTCTAGTACAAAGTGGGGACAAATAAAGTGGAAAGAGCTGCTCCAGACGCC 2594  
Db 301 CAGATTCCTCTAGTACAAAGTGGGGACAAATAAAGTGGAAAGAGCTGCTCCAGACGCC 360  
QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAAAAGAAATTTAGCTTCGAGCTCAG 2654  
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAAAAGAAATTTAGCTTCGAGCTCAG 420  
QY 2655 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714  
Db 421 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480  
QY 2715 AAATTTGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 2774  
Db 481 AAATTTGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 540  
QY 2775 TCGATATC 2782  
Db 541 TCGATATC 548

RESULT 9  
US-07-753-738B-6  
; Sequence 6, Application US/07753738B  
; Patent No. 5304730  
; GENERAL INFORMATION:  
; APPLICANT: Lawson, Edgar C.  
; APPLICANT: Weiss, James D.  
; APPLICANT: Hemenway, Cynthia L.  
; APPLICANT: Turner, Nilgun E.  
; TITLE OF INVENTION: Virus Resistant Plants and Method  
; TITLE OF INVENTION: Therefore  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/753,738B  
; FILING DATE: 19910903  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10536)A  
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-753-738B-6

Query Match 14.2%; Score 409.2; DB 2; Length 597;
Best Local Similarity 98.1%; Pred. No. 2.1e-80;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGAGTCTCCAAACCATTAGCCAAA 2294
Db 127 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGAGTCTCCAAACCATTAGCCAAA 186

QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTTGTTCAGCACATGCA 2354
Db 187 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTTGTTCAGCACATGCA 246

QY 2355 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 247 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 306

QY 2415 TTGAAAGTAATCTGTCAACATCGACAGCTGGCTTGTGGGACCGACACAAAAAGGAAT 2474
Db 307 TTGAAAGTAATCTGTCAACATCGACAGCTGGCTTGTGGGACCGACACAAAAAGGAAT 366

QY 2475 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCCAAAGATAAG 2534
Db 367 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCCAAAGATAAG 426

QY 2535 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTCTGACAGCC 2594
Db 427 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTCTGACAGCC 486

QY 2595 CACTCAGTAATCGGTATGACGACGACGAGTGGTGGGACCGACACCAAAAGATTAGCTTACGCTAG 2654
Db 487 CACTCAGTAATCGGTATGACGACGACGAGTGGTGGGACCGACACCAAAAGATTAGCTTACGCTAG 546

QY 2655 GA 2656
Db 547 AA 548

RESULT 10
US-08-368-260-4
; Sequence 4, Application US/08368260
; Patent No. 5503999
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.
; APPLICANT: Jilka, Joseph M.
; TITLE OF INVENTION: Virus Resistant Plants
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle D. Strode, Monsanto Co., BB4F
; STREET: 700 Chesterfield Parkway No. 5503999th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,260
; FILING DATE:
; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,416
; FILING DATE:
; APPLICATION NUMBER: US/07/910,224
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Strode, Janelle D.
; REGISTRATION NUMBER: 34,738
; REFERENCE/DOCKET NUMBER: 38-21(10550)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-368-260-4

Query Match 14.2%; Score 409.2; DB 2; Length 597;
Best Local Similarity 98.1%; Pred. No. 2.1e-80;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGAGTCTCCAAACCATTAGCCAAA 2294
Db 127 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGAGTCTCCAAACCATTAGCCAAA 186

QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTTGTTCAGCACATGCA 2354
Db 187 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTTGTTCAGCACATGCA 246

QY 2355 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 247 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 306

QY 2415 TTGAAAGTAATCTGTCAACATCGACAGCTGGCTTGTGGGACCGACACAAAAAGGAAT 2474
Db 307 TTGAAAGTAATCTGTCAACATCGACAGCTGGCTTGTGGGACCGACACAAAAAGGAAT 366

QY 2475 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCCAAAGATAAG 2534
Db 367 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCCAAAGATAAG 426

QY 2535 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTCTGACAGCC 2594
Db 427 CAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTCTGACAGCC 486

QY 2595 CACTCAGTAATCGGTATGACGACGACGAGTGGTGGGACCGACACCAAAAGATTAGCTTACGCTAG 2654
Db 487 CACTCAGTAATCGGTATGACGACGACGAGTGGTGGGACCGACACCAAAAGATTAGCTTACGCTAG 546

QY 2655 GA 2656
Db 547 AA 548

RESULT 11
US-07-809-457A-17
; Sequence 17, Application US/07809457A
; Patent No. 5512466
; GENERAL INFORMATION:
; APPLICANT: Klee, Harry J.
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
```

; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19911217  
; APPLICATION NUMBER: US/07/809,457A  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,440  
; FILING DATE: 26-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10538)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 597 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-809-457A-17

Query Match 14.2%; Score 409.2; DB 2; Length 597;

Best Local Similarity 98.1%; Pred. No. 2.1e-80;  
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	2235	AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	2294
Db	127	AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	186
QY	2295	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	2354
Db	187	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	246
QY	2355	TCATGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT	2414
Db	247	TCATGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT	306
QY	2535	CAGATTCTCTVAGTACAAAGTGGGAAACAAATAACGTTGGAAAGAGCTGCTTCACAGCC	2594
Db	427	CAGATTCTCTVAGTACAAAGTGGGAAACAAATAACGTTGGAAAGAGCTGCTTCACAGCC	486
QY	2595	CACCTCACTAATGCGTATGACGAAACGCGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG	2654
Db	487	CACCTCACTAATGCGTATGACGAAACGCGAGTACGACCAACAAAGAAATTTCCCTCTATATAAG	546
QY	2655	GA 2656	
Db	547	AA 548	

## RESULT 12

US-08-148-022-5  
; Sequence 5, Application US/08148022  
; Patent No. 5589612  
; GENERAL INFORMATION:  
; APPLICANT: Tumer, Nilgun E.

; APPLICANT: Jilka, Joseph M.  
; TITLE OF INVENTION: Virus Resistant Plants  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janelle D. Strode, Monsanto Co., BB4F  
; STREET: 700 Chesterfield Parkway No. 5589612th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/148,022  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/910,792  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Strode, Janelle D.  
; REGISTRATION NUMBER: 34,738  
; REFERENCE/DOCKET NUMBER: 38-21(10549)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 597 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-148-022-5

Query Match 14.2%; Score 409.2; DB 2; Length 597;

Best Local Similarity 98.1%; Pred. No. 2.1e-80;  
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	2235	AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	2294
Db	127	AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	186
QY	2295	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	2354
Db	187	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	246
QY	2355	TCATGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT	2414
Db	247	TCATGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT	306
QY	2415	TTGAAAGTAATCTTGTCAACATCGACAGCTGGCTTGTGGGACCGACACAAAAAGGAAT	2474
Db	307	TTGAAAGTAATCTTGTCAACATCGACAGCTGGCTTGTGGGACCGACACAAAAAGGAAT	366
QY	2475	GGTGCAGAAATTTAGTCGCGACCTTACCAAAAGCATCTTTCGCTTTATTGCAAGATAAAG	2534
Db	367	GGTGCAGAAATTTAGTCGCGACCTTACCAAAAGCATCTTTCGCTTTATTGCAAGATAAAG	426
QY	2535	CAGATTCTCTAGTACAAAGTGGGAAACAAATAACGTTGGAAAGAGCTGCTTCACAGCC	2594
Db	427	CAGATTCTCTAGTACAAAGTGGGAAACAAATAACGTTGGAAAGAGCTGCTTCACAGCC	486
QY	2595	CACCTCACTAATGCGTATGACGAAACGCGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG	2654
Db	487	CACCTCACTAATGCGTATGACGAAACGCGAGTACGACCAACAAAGAAATTTCCCTCTATATAAG	546
QY	2655	GA 2656	
Db	547	AA 548	



RESULT 13  
US-08-476-008-1  
; Sequence 1, Application US/08476008  
; Patent No. 5627061  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stallings, William C.  
; TITLE OF INVENTION: Glyphosate Tolerant  
; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,008  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,063  
; FILING DATE: 13-SEP-1994  
; APPLICATION NUMBER: US 07/749,611  
; FILING DATE: 28-AUG-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/576,537  
; FILING DATE: 31-AUG-1990  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10660)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 597 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-476-008-1  
Query Match 14.2%; Score 409.2; DB 2; Length 597;  
Best Local Similarity 98.1%; Pred. No. 2.1e-80;  
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTCCAGGTACAGAGTCTCCAAACATTAGCCAAA 2294  
DB 127 AATTCTCAGTCCAAAGCCTCAACAGGTCCAGGTACAGAGTCTCCAAACATTAGCCAAA 186  
QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAGTAACTACTGTTCCAGCACATGCA 2354  
DB 187 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAGTAACTACTGTTCCAGCACATGCA 246  
QY 2355 TCATGGTCAAGTAACTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414  
DB 247 TCATGGTCAAGTAACTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 306  
QY 2415 TTGAAAGTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAGGAAT 2474

DB 307 TTGAAAGTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAGGAAT 366  
QY 2475 GGTGAGAAATTTAGGCGCACCTACCAAAAAGCACTTTGGCCTTTATTGCAAGATAAAG 2534  
DB 367 GGTGAGAAATTTAGGCGCACCTACCAAAAAGCACTTTGGCCTTTATTGCAAGATAAAG 426  
QY 2535 CAGATTTCCTCTAGTACAGTGGGGACAAAATAAGCTGGAAGAGCTGCTCTGACAGCC 2594  
DB 427 CAGATTTCCTCTAGTACAGTGGGGACAAAATAAGCTGGAAGAGCTGCTCTGACAGCC 486  
QY 2595 CACTCACTAATCGGTATGACGAAACGAGTACGACCAACAAAAGAAATTAGCTTGAAGCTCAG 2654  
DB 487 CACTCACTAATCGGTATGACGAAACGAGTACGACCAACAAAAGAAATTCCCTCTATATAAG 546  
QY 2655 GA 2656  
DB 547 AA 548  
RESULT 14  
US-08-306-063-1  
; Sequence 1, Application US/08306063  
; Patent No. 5633435  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stallings, William C.  
; TITLE OF INVENTION: Glyphosate Tolerant  
; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,063  
; FILING DATE: 13-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,611  
; FILING DATE: 28-AUG-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/576,537  
; FILING DATE: 31-AUG-1990  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10660)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 597 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-306-063-1  
Query Match 14.2%; Score 409.2; DB 2; Length 597;



	Best Local Similarity	98.1%;	Pred: No. 2.1e-80;		0;					
	Matches	414;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;
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Db	127	AATTC	CAGTCCAAAGCCTCAACAAGGTCAAGGTCAAGGTCTCCAAACCATTTAGCCAAA	186						
QY	2295	AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTGTTTCAGACACATGCA	2354							
Db	187	AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTGTTTCAGACACATGCA	246							
QY	2355	TCATGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT	2414							
Db	247	TCATGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT	306							
QY	2415	TTGAAAGTAACTTTGTCAACATCGACGAGCTGGCTTTGTGGGGACCGACAGACAAAAAGGAAT	2474							
Db	307	TTGAAAGTAACTTTGTCAACATCGACGAGCTGGCTTTGTGGGGACCGACAGACAAAAAGGAAT	366							
QY	2475	GGTGCAGAAATTGTTAGCGGCACCTACCAAAGACATCTTTGCCCTTTATTGCAAGATAAAG	2534							
Db	367	GGTGCAGAAATTGTTAGCGGCACCTACCAAAGACATCTTTGCCCTTTATTGCAAGATAAAG	426							
QY	2535	CAGATTCTCTAGTACAAAGTGGGGACAAATAACGTGGAAAAAGAGCTGTCCTGCACAGCC	2594							
Db	427	CAGATTCTCTAGTACAAAGTGGGGACAAATAACGTGGAAAAAGAGCTGTCCTGCACAGCC	486							
QY	2595	CAGTCACTAATGCGTATGACGAACGCGAGTCACGACCAACAAAGAAATTTAGCTTCGAGCTCAG	2654							
Db	487	CAGTCACTAATGCGTATGACGAACGCGAGTCACGACCAACAAAGAAATTTCCCTCTATATAAG	546							
QY	2655	GA	2656							
Db	547	AA	548							

Search completed: March 30, 2006, 14:53:01  
Job time : 952.807 secs

RESULT 15  
US-08-553-943-17  
; Sequence 17, Application US/08553943  
; Patent No. 5702933  
; GENERAL INFORMATION:  
; APPLICANT: Klee, Harry J.  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence  
; TITLE OF INVENTION: in Plants  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Monsanto Co. B44F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,943  
; FILING DATE: 06-NOV-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/809,457  
; FILING DATE: 17-DEC-1991  
; APPLICATION NUMBER: US 07/632,440  
; FILING DATE: 26-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10538)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099



Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	646	22.4	1695	6	US-10-427-169-28	Sequence 28, Appl
3	646	22.4	1695	6	US-10-427-180-28	Sequence 28, Appl
4	646	22.4	1695	8	US-10-909-860-28	Sequence 28, Appl
5	646	22.4	1695	8	US-10-920-869-28	Sequence 28, Appl
6	556	19.3	5822	3	US-09-924-197-1	Sequence 1, Appl
7	548	19.0	1946	3	US-09-737-626A-27	Sequence 27, Appl
8	548	19.0	1946	6	US-10-427-169-27	Sequence 27, Appl
9	548	19.0	1946	6	US-10-427-180-27	Sequence 27, Appl
10	548	19.0	1946	8	US-10-909-860-27	Sequence 27, Appl
11	548	19.0	1946	8	US-10-920-869-27	Sequence 27, Appl
12	409.2	14.2	597	3	US-09-861-696-1	Sequence 1, Appl
13	409.2	14.2	597	3	US-09-464-099A-1	Sequence 1, Appl
14	409.2	14.2	1042	7	US-10-376-763A-17	Sequence 17, Appl
15	409.2	14.2	1630	5	US-10-213-791-23	Sequence 23, Appl
16	409.2	14.2	3706	7	US-10-376-763A-6	Sequence 6, Appl
17	409.2	14.2	3778	7	US-10-376-763A-5	Sequence 5, Appl
18	409.2	14.2	10846	3	US-09-923-109-5	Sequence 5, Appl
19	409.2	14.2	10846	6	US-10-164-204-5	Sequence 5, Appl
20	409.2	14.2	10846	7	US-10-705-430-5	Sequence 5, Appl
21	409.2	14.2	10900	3	US-09-923-109-6	Sequence 6, Appl
22	409.2	14.2	10900	6	US-10-164-204-6	Sequence 6, Appl
23	409.2	14.2	10900	7	US-10-705-430-6	Sequence 6, Appl



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Db      61  AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAATCTAGTTTCAGACATGCA 120
QY      2355  TCATGGTCAGTAACTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGATCT 2414
Db      121  TCATGGTCAGTAACTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGATCT 180
QY      2415  TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAGGAAT 2474
Db      181  TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAGGAAT 240
QY      2475  GGTGCGAATTTGTAGCGCACCTTACAAAAGCATCTTTCGCTTTATTTGCAAGATAAG 2534
Db      241  GGTGCGAATTTGTAGCGCACCTTACAAAAGCATCTTTCGCTTTATTTGCAAGATAAG 300
QY      2535  CAGATTCTCTAGTACAAAGTGGGGAACAAAATAACCGTGGAAAAGAGCTGCTCGACAGCC 2594
Db      301  CAGATTCTCTAGTACAAAGTGGGGAACAAAATAACCGTGGAAAAGAGCTGCTCGACAGCC 360
QY      2595  CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACCAAGGATAGCTTGGAGTCTAG 2654
Db      361  CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACCAAGGATAGCTTGGAGTCTAG 420
QY      2655  GATTAGCAGATTCAGATTGGTTCATCAACAGGATAGGAGCCATATCATTATTTC 2714
Db      421  GATTAGCAGATTCAGATTGGTTCATCAACAGGATAGGAGCCATATCATTATTTC 480
QY      2715  AAATTGGTATCGCCAAACCAAGGAAGAACTCCCATCTCCAAAGGTTTGTAAAGAGAAT 2774
Db      481  AAATTGGTATCGCCAAACCAAGGAAGAACTCCCATCTCCAAAGGTTTGTAAAGAGAAT 540
QY      2775  TCGATATCAAGCTTGATATCGGAAGTTTCTCTTTGAGGGAGGTTGCTCGTGAATGGGA 2834
Db      541  TCGATATCAAGCTTGATATCGGAAGTTTCTCTTTGAGGGAGGTTGCTCGTGAATGGGA 600
QY      2835  CACATATGGTTGTTATATAAACCAATTTCCATTTGTCATGAGATTTT 2880
Db      601  CACATATGGTTGTTATATAAACCAATTTCCATTTGTCATGAGATTTT 646

RESULT 4
US-10-909-860-28
; Sequence 28, Application US/10909860
; Publication No. US2005005332A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/909,860
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EFl polynucleotides + EFl intron
; US-10-909-860-28

Query Match      22.4%; Score 646; DB 8; Length 1695;
Best Local Similarity 100.0%; Pred. No. 3.9e-115;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2235  AATTCTCAGTCCAAAGCCTCAACAGGTCAGGGTACAGAGTCTCCAAACCAATTAGCCAAA 2294
Db      1  AATTCTCAGTCCAAAGCCTCAACAGGTCAGGGTACAGAGTCTCCAAACCAATTAGCCAAA 60
QY      2295  AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGACATGCA 2354
Db      61  AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGACATGCA 120
QY      2355  TCATGGTCAGTAACTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGATCT 2414
Db      121  TCATGGTCAGTAACTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGATCT 180
QY      2415  TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAGGAAT 2474
Db      181  TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAGGAAT 240
QY      2475  GGTGCGAATTTGTAGCGCACCTTACAAAAGCATCTTTCGCTTTATTTGCAAGATAAG 2534
Db      241  GGTGCGAATTTGTAGCGCACCTTACAAAAGCATCTTTCGCTTTATTTGCAAGATAAG 300
QY      2535  CAGATTCTCTAGTACAAAGTGGGGAACAAAATAACCGTGGAAAAGAGCTGCTCGACAGCC 2594
Db      301  CAGATTCTCTAGTACAAAGTGGGGAACAAAATAACCGTGGAAAAGAGCTGCTCGACAGCC 360
QY      2595  CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACCAAGGATAGCTTGGAGTCTAG 2654
Db      361  CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACCAAGGATAGCTTGGAGTCTAG 420
QY      2655  GATTAGCAGATTCAGATTGGTTCATCAACAGGATAGGAGCCATATCATTATTTC 2714
Db      421  GATTAGCAGATTCAGATTGGTTCATCAACAGGATAGGAGCCATATCATTATTTC 480
QY      2715  AAATTGGTATCGCCAAACCAAGGAAGAACTCCCATCTCCAAAGGTTTGTAAAGAGAAT 2774
Db      481  AAATTGGTATCGCCAAACCAAGGAAGAACTCCCATCTCCAAAGGTTTGTAAAGAGAAT 540
QY      2775  TCGATATCAAGCTTGATATCGGAAGTTTCTCTTTGAGGGAGGTTGCTCGTGAATGGGA 2834
Db      541  TCGATATCAAGCTTGATATCGGAAGTTTCTCTTTGAGGGAGGTTGCTCGTGAATGGGA 600
QY      2835  CACATATGGTTGTTATATAAACCAATTTCCATTTGTCATGAGATTTT 2880
Db      601  CACATATGGTTGTTATATAAACCAATTTCCATTTGTCATGAGATTTT 646

RESULT 5
US-10-920-869-28
; Sequence 28, Application US/10920869
; Publication No. US2005002261A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/920,869
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EFl polynucleotides + EFl intron
; US-10-920-869-28

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Query Match 22.4%; Score 646; DB 8; Length 1695;  
Best Local Similarity 100.0%; Pred. No. 3.9e-115;  
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTCAGGTCAGAGTCTCCAAAGCATTAGCCAA 2294  
DB 1 AATTCTCAGTCCAAAGCCTCAACAGGTCAGGTCAGAGTCTCCAAAGCATTAGCCAA 60

QY 2295 AGCTACAGGAGTCAATGAAGAACTTCAATCAAGTAACTACTGTTTCAGCACATGCA 2354  
DB 61 AGCTACAGGAGTCAATGAAGAACTTCAATCAAGTAACTACTGTTTCAGCACATGCA 120

QY 2355 TCATGTCAGTAACTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGCATCT 2414  
DB 121 TCATGTCAGTAACTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGCATCT 180

QY 2415 TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGGAAT 2474  
DB 181 TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGGAAT 240

QY 2475 GGTGCAGAAATTGTAGGCGCAGCTACCAAAAGCATCTTTGCCCTTTATTCGAAAGTAAAG 2534  
DB 241 GGTGCAGAAATTGTAGGCGCAGCTACCAAAAGCATCTTTGCCCTTTATTCGAAAGTAAAG 300

QY 2535 CAGATTCCTCTAGTCAAGTGGGACCAAAATTAACGTGGAAAGAGCTGTCTGCAGCC 2594  
DB 301 CAGATTCCTCTAGTCAAGTGGGACCAAAATTAACGTGGAAAGAGCTGTCTGCAGCC 360

QY 2595 CACTCACTAATCGGTATGACGACGAGTACGACCAACCAAAAGAAATTTAGCTTGTAGCTCAG 2654  
DB 361 CACTCACTAATCGGTATGACGACGAGTACGACCAACCAAAAGAAATTTAGCTTGTAGCTCAG 420

QY 2655 GATTAGAGCATTCAGATTTGGTTTCAATCAACAGGTACGAGCCATATCATCTTTATTC 2714  
DB 421 GATTAGAGCATTCAGATTTGGTTTCAATCAACAGGTACGAGCCATATCATCTTTATTC 480

QY 2715 AAATGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGTTTGTAGGAGAAAT 2774  
DB 481 AAATGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGTTTGTAGGAGAAAT 540

QY 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTGCTCGTGGAAATGGGA 2834  
DB 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTGCTCGTGGAAATGGGA 600

QY 2835 CACATATGTTGTTATATAAACCATTTCATTTGTCATGAGATTTT 2880  
DB 601 CACATATGTTGTTATATAAACCATTTCATTTGTCATGAGATTTT 646

RESULT 6  
US-09-924-197-1  
; Sequence 1, Application US/09924197  
; Publication No. US20030018993A1  
; GENERAL INFORMATION:  
; APPLICANT: Gutterson, Neal  
; APPLICANT: Oeller, Paul  
; TITLE OF INVENTION: Improved Methods of Gene Silencing Using Inverted  
; TITLE OF INVENTION: Repeat Sequences  
; FILE REFERENCE: 012176-010810US  
; CURRENT APPLICATION NUMBER: US/09/924,197  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 60/225,508  
; PRIOR FILING DATE: 2000-08-15  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 5822  
; TYPE: DNA  
; ORGANISM: Agrobacterium tumefaciens  
US-09-924-197-1

Query Match 19.3%; Score 556; DB 3; Length 5822;

Best Local Similarity 99.1%; Pred. No. 2e-97;  
Matches 559; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2221 CTCAGTGGAGCTAATTTCTCAGTCCAAAGCCTCAACAGGTCAGGTTACAGAGTCTCCA 2280  
DB 284 CTCAGTGGAGCTAATTTCTCAGTCCAAAGCCTCAACAGGTCAGGTTACAGAGTCTCCA 343

QY 2281 ACCATTAGCCAAAGGCTACAGGAGTCAATGAAGAACTTCAATCAAGTAACTACTG 2340  
DB 344 AACCATTAGCCAAAGGCTACAGGAGTCAATGAAGAACTTCAATCAAGTAACTACTG 403

QY 2341 TTCCAGCACATGCATCATGGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAA 2400  
DB 404 TTCCAGCACATGCATCATGGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAA 463

QY 2401 GTTAGTGGGCACTTTTGAAGAACTTGTTCAACTCGAGCAGCTGGCTTTGTGGGACCA 2460  
DB 464 GTTAGTGGGCACTTTTGAAGAACTTGTTCAACTCGAGCAGCTGGCTTTGTGGGACCA 523

QY 2461 GACAAAAAGGAATGGTCAGAAATTTGTAGGCGCACCTTACCAAAAGCATCTTTGCCCTTTA 2520  
DB 524 GACAAAAAGGAATGGTCAGAAATTTGTAGGCGCACCTTACCAAAAGCATCTTTGCCCTTTA 583

QY 2521 TTGCAAGATAAGCAGAGTTCCTCTAGTACAAAGTGGGAAACAAAATAACGTGAAAAGAG 2580  
DB 584 TTGCAAGATAAGCAGAGTTCCTCTAGTACAAAGTGGGAAACAAAATAACGTGAAAAGAG 643

QY 2581 CTGTCTCGACAGCCCACTCACTAAATGCGTATGCGAAACGCGAGTACGACCAACAAAGAA 2640  
DB 644 CTGTCTCGACAGCCCACTCACTAAATGCGTATGCGAAACGCGAGTACGACCAACAAAGAA 703

QY 2641 TAGCTTGAGCTCAGGATTTAGCAGCATTTCCAGATTGGGTTCAATCAAGGTTACGAGCC 2700  
DB 704 TAGCTTGAGCTCAGGATTTAGCAGCATTTCCAGATTGGGTTCAATCAAGGTTACGAGCC 763

QY 2701 ATATCACTTTATTCAAATTTGGTATCGCAAAACCAAGAGGAACTCCCATCTCTCAAAGGT 2760  
DB 764 ATATCACTTTATTCAAATTTGGTATCGCAAAACCAAGAGGAACTCCCATCTCTCAAAGGT 823

QY 2761 TTGTAAGGAAGAAATTCGATATCAA 2784  
DB 824 TTGTAAGGAAGAAATTCGATATCAA 847

RESULT 7  
US-09-737-626A-27  
; Sequence 27, Application US/09737626A  
; Patent No. US20020144304A1  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen  
; APPLICANT: Flisinski, Stanislaw  
; APPLICANT: Wilkinson, Jack  
; TITLE OF INVENTION: No. US20020144304A1el Plant Expression Constructs  
; FILE REFERENCE: 38-21(51499)B  
; CURRENT APPLICATION NUMBER: US/09/737,626A  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 09/737,626  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 1946  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)-(1946)  
; OTHER INFORMATION: chimeric promoter fusion PMV and Act11 polynucleotides + Act11  
; OTHER INFORMATION: ntro  
US-09-737-626A-27

Query Match 19.0%; Score 548; DB 3; Length 1946;  
Best Local Similarity 100.0%; Pred. No. 4.5e-96;

Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTCTCCAAACCATTAGCCAAA 2294  
 Db 1 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTCTCCAAACCATTAGCCAAA 60

QY 2295 AGCTACAGGAGATCAATGAAGAACTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA 2354  
 Db 61 AGCTACAGGAGATCAATGAAGAACTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA 120

QY 2355 TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414  
 Db 121 TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180

QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGCAAAAAAGGAAT 2474  
 Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGCAAAAAAGGAAT 240

QY 2475 GGTGCAGAAATTTAGGGCCACCTACCAAAAGCATCTTGGCTTTATTGCAAGATAAAG 2534  
 Db 241 GGTGCAGAAATTTAGGGCCACCTACCAAAAGCATCTTGGCTTTATTGCAAGATAAAG 300

QY 2535 CAGATTCCTCTAGTACAAAGTGGGGAACAAATTAACGTGGAAGAGCTGCTGCACAGCC 2594  
 Db 301 CAGATTCCTCTAGTACAAAGTGGGGAACAAATTAACGTGGAAGAGCTGCTGCACAGCC 360

QY 2595 CACTCACTAATGCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 2654  
 Db 361 CACTCACTAATGCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 420

QY 2655 GATTTAGCAGCATTTCCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 2714  
 Db 421 GATTTAGCAGCATTTCCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 480

QY 2715 AAATTGGTATCGCCAAAACCAAGGAAGAACTCCCATCTCTCAAGAGTTTGTAAAGGAAGAAT 2774  
 Db 481 AAATTGGTATCGCCAAAACCAAGGAAGAACTCCCATCTCTCAAGAGTTTGTAAAGGAAGAAT 540

QY 2775 TCGATATC 2782  
 Db 541 TCGATATC 548

RESULT 8

US-10-427-169-27

; Sequence 27, Application US/10427169

; Publication No. US20030199681A1

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen

; APPLICANT: Flasiniski, Stanislaw

; APPLICANT: Wilkinson, Jack

; TITLE OF INVENTION: No. US20030199681A1 Plant Expression Constructs

; FILE REFERENCE: 38-21(51499)B

; CURRENT APPLICATION NUMBER: US/10/427,169

; PRIOR FILING DATE: 2003-05-01

; PRIOR APPLICATION NUMBER: US/09/737,626A

; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: 09/737,626

; PRIOR FILING DATE: 2000-12-15

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 27

; LENGTH: 1946

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: promoter

; LOCATION: (1)..(1946)

; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides + Act11

; OTHER INFORMATION: ntro

US-10-427-169-27

Query Match 19.0%; Score 548; DB 6; Length 1946;

Best Local Similarity 100.0%; Pred. No. 4.5e-96;

Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTCTCCAAACCATTAGCCAAA 2294  
 Db 1 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTCTCCAAACCATTAGCCAAA 60

QY 2295 AGCTACAGGAGATCAATGAAGAACTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA 2354  
 Db 61 AGCTACAGGAGATCAATGAAGAACTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA 120

QY 2355 TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414  
 Db 121 TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180

QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGCAAAAAAGGAAT 2474  
 Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGCAAAAAAGGAAT 240

QY 2475 GGTGCAGAAATTTAGGGCCACCTACCAAAAGCATCTTGGCTTTATTGCAAGATAAAG 2534  
 Db 241 GGTGCAGAAATTTAGGGCCACCTACCAAAAGCATCTTGGCTTTATTGCAAGATAAAG 300

QY 2535 CAGATTCCTCTAGTACAAAGTGGGGAACAAATTAACGTGGAAGAGCTGCTGCACAGCC 2594  
 Db 301 CAGATTCCTCTAGTACAAAGTGGGGAACAAATTAACGTGGAAGAGCTGCTGCACAGCC 360

QY 2595 CACTCACTAATGCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 2654  
 Db 361 CACTCACTAATGCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTGAGCTCAG 420

QY 2655 GATTTAGCAGCATTTCCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 2714  
 Db 421 GATTTAGCAGCATTTCCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 480

QY 2715 AAATTGGTATCGCCAAAACCAAGGAAGAACTCCCATCTCTCAAGAGTTTGTAAAGGAAGAAT 2774  
 Db 481 AAATTGGTATCGCCAAAACCAAGGAAGAACTCCCATCTCTCAAGAGTTTGTAAAGGAAGAAT 540

QY 2775 TCGATATC 2782  
 Db 541 TCGATATC 548

RESULT 9

US-10-427-180-27

; Sequence 27, Application US/10427180

; Publication No. US20030199682A1

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen

; APPLICANT: Flasiniski, Stanislaw

; APPLICANT: Wilkinson, Jack

; TITLE OF INVENTION: No. US20030199682A1 Plant Expression Constructs

; FILE REFERENCE: 38-21(51499)B

; CURRENT APPLICATION NUMBER: US/10/427,180

; CURRENT FILING DATE: 2003-05-01

; PRIOR APPLICATION NUMBER: US/09/737,626A

; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: 09/737,626

; PRIOR FILING DATE: 2000-12-15

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 27

; LENGTH: 1946

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: promoter

; LOCATION: (1)..(1946)

; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides + Act11

; OTHER INFORMATION: ntro

US-10-427-180-27

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Query Match      19.0%; Score 548; DB 6; Length 1946;
Best Local Similarity 100.0%; Pred. No. 4.5e-96;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

QY 2295 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 120

QY 2355 TCATGGTCAAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCAAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 180

QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 240

QY 2475 GGTGCAGAAATTGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 2534
Db 241 GGTGCAGAAATTGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300

QY 2535 CAGATTCCCTAGTACAAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTTCGACAGCC 2594
Db 301 CAGATTCCCTAGTACAAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTTCGACAGCC 360

QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGGCTCAG 2654
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGGCTCAG 420

QY 2655 GATTTAGCAGCATTCAGATTTGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTTAGCAGCATTCAGATTTGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480

QY 2715 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTAAAGAAAGAT 2774
Db 481 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTAAAGAAAGAT 540

QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 10
US-10-909-860-27
; Sequence 27, Application US/10909860
; Publication No. US20050005332A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasinaki, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/909,860
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +
; OTHER INFORMATION: ntro
US-10-909-860-27
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Query Match      19.0%; Score 548; DB 8; Length 1946;
Best Local Similarity 100.0%; Pred. No. 4.5e-96;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

QY 2295 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 120

QY 2355 TCATGGTCAAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCAAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 180

QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 240

QY 2475 GGTGCAGAAATTGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 2534
Db 241 GGTGCAGAAATTGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300

QY 2535 CAGATTCCCTAGTACAAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTTCGACAGCC 2594
Db 301 CAGATTCCCTAGTACAAAGTGGGGAACAAAATAACGTGGAAAGAGCTGTCTTCGACAGCC 360

QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGGCTCAG 2654
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGGCTCAG 420

QY 2655 GATTTAGCAGCATTCAGATTTGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTTAGCAGCATTCAGATTTGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480

QY 2715 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTAAAGAAAGAT 2774
Db 481 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTAAAGAAAGAT 540

QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 11
US-10-920-869-27
; Sequence 27, Application US/10920869
; Publication No. US2005002261A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasinaki, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/920,869
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +
; OTHER INFORMATION: ntro
US-10-920-869-27
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QY 2355 TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
264 TCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 323
QY 2415 TTGAAAGTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACCGACACAAAAGGAAT 2474
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
324 TTGAAAGTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACCGACACAAAAGGAAT 383
QY 2475 GGTGCAGAAATTGTTAGGCGCACCTTACCAAAAGCATCTTTGCCTTTATTGCAAAAGATAAAG 2534
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
384 GGTGCAGAAATTGTTAGGCGCACCTTACCAAAAGCATCTTTGCCTTTATTGCAAAAGATAAAG 443
QY 2535 CAGATTCCTCTAGTACAAAGTGGGGAACAAAATAACGTGGAAAAAGAGCTGCTGCACAGCC 2594
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
444 CAGATTCCTCTAGTACAAAGTGGGGAACAAAATAACGTGGAAAAAGAGCTGCTGCACAGCC 503
QY 2595 CACTCACTAATGCGTATGACGAACGCGAGTGCAGCAGCAGCAACAAAGAAATTAGCTTGAGCTCAG 2654
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
504 CACTCACTAATGCGTATGACGAACGCGAGTGCAGCAGCAGCAACAAAGAAATTCCTCTATATAG 563
QY 2655 GA 2656
Db 564 AA 565
```

Search completed: March 31, 2006, 07:57:46  
Job time : 2214.86 secs

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:01:03 ; Search time 1107.43 Seconds  
(without alignments)  
10080.402 Million cell updates/sec

Title: US-10-541-346-4

Perfect score: 1675

Sequence: 1 tgcaccgaagtaatatgagg.....tagtgcgaacctggagaag 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	1675	13	ADR46166
2	530.6	31.7	3706	13	ADR49368
3	530.6	31.7	3778	13	ADR49367
4	312.8	18.7	7794	14	AEB71496
5	310	18.5	8012	2	AAx57305
6	310	18.5	8418	2	AAx57309
7	310	18.5	8798	2	AAx57308
8	310	18.5	10846	6	ABs54336
9	310	18.5	10847	2	AAx08923
10	310	18.5	10900	2	AAx08924
11	310	18.5	10900	2	ABs54337
12	310	18.5	11606	12	ADQ13598
13	295	17.6	662	14	ADW69411
14	295	17.6	1998	8	ABV76269
15	289	17.3	12304	8	ABV75876
16	289	17.3	12497	8	ABV75875
17	289	17.3	12614	4	AAc66931
18	282	16.8	632	6	ABN83922
19	280.2	16.7	5365	13	ADU73233

20	280.2	16.7	7713	12	ADQ95182
21	280.2	16.7	7794	14	AEB71496
22	280.2	16.7	8179	12	ADQ95181
23	280.2	16.7	8590	14	AEB71495
24	280.2	16.7	10249	3	AAAL5563
25	280.2	16.7	10312	3	AAAL5564
26	280.2	16.7	10339	3	AAAL5562
c 27	280.2	16.7	10390	6	ABL54627
c 28	280.2	16.7	12739	14	ADW39084
c 29	280.2	16.7	14194	4	AAc66932
c 30	280.2	16.7	15397	2	AAc58635
c 31	280.2	16.7	17511	14	ADV39061
c 32	280.2	16.7	18987	14	ADV39062
c 33	280.2	16.7	24596	1	AAAN50182
c 34	280	16.7	1461	14	AEA89731
c 35	280	16.7	7450	14	AEA89733
c 36	278.8	16.6	10603	13	ADU69212
c 37	278.6	16.6	10078	6	ABO73047
c 38	278.6	16.6	24593	1	AAAN50226
c 39	271.4	16.2	10575	13	ADU69210
c 40	271.4	16.2	10677	13	ADU69211
c 41	270.2	16.1	10323	2	AAx90954
c 42	270.2	16.1	15676	3	AAAD01288
c 43	270.2	16.1	17111	3	AAAD01289
c 44	270.2	16.1	17116	3	AAAD01290
45	268.2	16.0	550	13	ADT03989

#### ALIGNMENTS

#### RESULT 1

ADR46166

ID ADR46166 standard; DNA; 1675 BP.

XX ADR46166;

XX 18-NOV-2004 (first entry)

XX Glyphosate resistance cotton event MON 88913 3' DNA junction sequence.

XX Glyphosate tolerance; herbicide tolerance; cotton; transgenic; plant;

XX MON 88913; gene; ds.

XX Gossypium hirsutum.

XX Agrobacterium sp.

XX Chimeric.

XX Key Location/Qualifiers

XX misc\_difference 600..601

XX /\*tag= a

XX /note= "3' junction of transgene and genomic DNA"

XX WO2004072235-A2.

XX 26-AUG-2004.

XX 02-FEB-2004; 2004WO-US002907.

XX 12-FEB-2003; 2003US-0447184P.

XX (MONS ) MONSANTO TECHNOLOGY LLC.

XX Cerny RE, Duong C, Hart JL, Huber SA, Krieb RL, Listello JJ;

XX Martens AB, Sammons B;

XX WPI; 2004-625846/60.

XX New seed of cotton event designated MON 88913, useful for producing a

XX cotton plant that tolerates application of glyphosate herbicide to

XX control weeds in crop.

XX Claim 5; SEQ ID NO 4; 50pp; English.

XX The present sequence is the 3' transgene/genomic junction sequence of  
CC glyphosate tolerant cotton event MON 88913. This sequence is novel in  
CC cotton event MON 88913. A cotton plant and seed comprising the sequence  
CC in its genome is an aspect of the invention. Cotton event MON 88913 was  
CC generated by an Agrobacterium-mediated transformation of cotton cells  
CC with a DNA fragment derived from pMON51915. The DNA fragment contained 2  
CC transgene expression cassettes that each included a glyphosate tolerant 5  
CC -enol-pyruvylisohikimate-3-phosphate synthase (EPSPS) sequence from  
CC Agrobacterium sp. strain CP4. The invention is related to the transgenic  
CC cotton event MON 88913 having seed deposited at ATCC PTA-4854, and to  
CC progeny plants and seeds or their regenerable parts, and cotton plants  
CC having a glyphosate tolerant phenotype. Methods are also provided for  
CC detecting the presence of DNA corresponding to cotton event MON 88913 in  
CC a sample by detecting a transgene/genomic junction region from cotton  
CC plant event MON 88913. A DNA primer comprising at least 11 contiguous  
CC nucleotides homologous of the present sequence, or its complement, is  
CC used in a DNA amplification method to produce an amplicon comprising the  
CC 3' junction region ADR46164 diagnostic for cotton event MON 88913. Also  
CC provided are methods of producing glyphosate tolerant cotton plants, a  
CC method for determining the zygosity of the progeny of cotton event MON  
CC 88913, and a method for controlling weeds in a crop or field of cotton  
CC event MON 88913 by applying glyphosate herbicide.  
XX  
SQ Sequence 1675 BP; 633 A; 221 C; 190 G; 631 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 1675; DB 13; Length 1675;  
Best Local Similarity 100.0%; Pred. No. 1.5e-185;  
Matches 1675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TGACCGAGTTAATGAGGAGTAAACACTTGTAGTGTGACCATTTGCTTATTCACCTA 60  
DB 1 TGACCGAGTTAATGAGGAGTAAACACTTGTAGTGTGACCATTTGCTTATTCACCTA 60  
  
QY 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAATGTTTACTGCAATACAGTATGTC 120  
DB 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAATGTTTACTGCAATACAGTATGTC 120  
  
QY 121 CTCTGTGTTTATGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCCAG 180  
DB 121 CTCTGTGTTTATGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCCAG 180  
  
QY 181 ATTCTAATCATCTCTTTTAAATATATAGTTATCTCATGATTTGTTAGTGTAGTATGAAA 240  
DB 181 ATTCTAATCATCTCTTTTAAATATATAGTTATCTCATGATTTGTTAGTGTAGTATGAAA 240  
  
QY 241 TATTTTAAATGATTTATGACTTGCCTGCAATGATGCAACATGATCAATCGACTGC 300  
DB 241 TATTTTAAATGATTTATGACTTGCCTGCAATGATGCAACATGATCAATCGACTGC 300  
  
QY 301 AGCCACTCGAGTGGAGCCCTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTGCA 360  
DB 301 AGCCACTCGAGTGGAGCCCTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTGCA 360  
  
QY 361 AATAAGATTTCCGAATTAGAATAATTTGTTATGCTTTCGCTTAAATACGCGGAT 420  
DB 361 AATAAGATTTCCGAATTAGAATAATTTGTTATGCTTTCGCTTAAATACGCGGAT 420  
  
QY 421 CGTAAATTTGCTTTTATCAAAATGATCTTTCATTTTATAAATACGCTGCGACATCTAC 480  
DB 421 CGTAAATTTGCTTTTATCAAAATGATCTTTCATTTTATAAATACGCTGCGACATCTAC 480  
  
QY 481 ATTTTGAATGAAAAAATTTGGTAAATTAATCTCTTTTCTCCATATGTGACCATCAT 540  
DB 481 ATTTTGAATGAAAAAATTTGGTAAATTTGTTATGCTTTCCTTATTTGACCATCAT 540  
  
QY 541 ACTCATTTGCTGATCCATGTAGATTTCCGACATGAGCCATTTTCAATTTGAATATAT 600  
DB 541 ACTCATTTGCTGATCCATGTAGATTTCCGACATGAGCCATTTTCAATTTGAATATATAT 600  
  
QY 601 TACAAAGCTATTTGCTTTATACATATGCGAAAAATTTTGTACTATTAATCAGGGGTAAAT 660  
DB 601 TACAAAGCTATTTGCTTTATACATATGCGAAAAATTTTGTACTATTAATCAGGGGTAAAT 660

RESULT 2  
ADR49368  
ID ADR49368 standard; DNA; 3706 BP.

QY 661 TAGGAGGGGGCTTGTAGGCTCGCTTCTTAAATGAAAAATTTTCTATTAGTTATTT 720  
DB 661 TAGGAGGGGGCTTGTAGGCTCGCTTCTTAAATGAAAAATTTTCTATTAGTTATTT 720  
  
QY 721 AAAATTTTAAAAAGTAAATATATAAAATTTTCATTTAATCCTTTAAAAAATATAAAGATATA 780  
DB 721 AAAATTTTAAAAAGTAAATATATAAAATTTTCATTTAATCCTTTAAAAAATATAAAGATATA 780  
  
QY 781 GACTATTAATATGATGAATTAACAATTTTATCATATAAAATATAAATTTAATTTTCGAC 840  
DB 781 GACTATTAATATGATGAATTAACAATTTTATTTATCATATAAAATATAAATTTAATTTTCGAC 840  
  
QY 841 CCTTAACAAAATTTTCTGATTTTGGCCCTTAACGTAAATTTTGTATAAAACAATTTTCTT 900  
DB 841 CCTTAACAAAATTTTCTGATTTTGGCCCTTAACGTAAATTTTGTATAAAACAATTTTCTT 900  
  
QY 901 TTTGCAATTAATGATTTCTTTAATTCAGTCCCAAGAAAGAAATTTTATAATTCGATATGCG 960  
DB 901 TTTGCAATTAATGATTTCTTTAATTCAGTCCCAAGAAAGAAATTTTATAATTCGATATGCG 960  
  
QY 961 AAAGTTAGTCTTGGCTAGTGATATTAAGAGGAAAGAAACATATAAATCAATAAATTAATTT 1020  
DB 961 AAAGTTAGTCTTGGCTAGTGATATTAAGAGGAAAGAAACATATAAATCAATAAATTAATTT 1020  
  
QY 1021 TTAAGCAAAATAGTAAATTAAGGAAAGAAATTTCTACGATAGTCTATAATTCAAAAAAG 1080  
DB 1021 TTAAGCAAAATAGTAAATTAAGGAAAGAAATTTCTACGATAGTCTATAATTCAAAAAAG 1080  
  
QY 1081 AAATAATATCTTTAAACCAATTCGAAATTTTAAAAATACATCAGAAATATCTATTATTAAAT 1140  
DB 1081 AAATAATATCTTTAAACCAATTCGAAATTTTAAAAATACATCAGAAATATCTATTATTAAAT 1140  
  
QY 1141 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1200  
DB 1141 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1200  
  
QY 1201 AATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260  
DB 1201 AATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260  
  
QY 1261 ATATATTTTATACAGACATATAGAAATATAAATAAATAAATAAATAAATAAATAAATAA 1320  
DB 1261 ATATATTTTATACAGACATATAGAAATATAAATAAATAAATAAATAAATAAATAAATAA 1320  
  
QY 1321 TTTAATTTTAAACATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1380  
DB 1321 TTTAATTTTAAACATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1380  
  
QY 1381 AATTTTATTAATATATTTTATCAGATAATGCGATTTTATTTTACCTATATATAGATGACAT 1440  
DB 1381 AATTTTATTAATATATTTTATCAGATAATGCGATTTTATTTTACCTATATATAGATGACAT 1440  
  
QY 1441 AATCTACTTTTAAATTAAGTCTTAAATAATATATATCATACCAAAAAAATTTCTTAAATATGA 1500  
DB 1441 AATCTACTTTTAAATTAAGTCTTAAATAATATATATCATACCAAAAAAATTTCTTAAATATGA 1500  
  
QY 1501 ATCTGATAATATCTTAAACCCCTTTTATPAAAAAATCTTAAACCCCTTATATATTTTAAATTT 1560  
DB 1501 ATCTGATAATATCTTAAACCCCTTTTATPAAAAAATCTTAAACCCCTTATATATTTTAAATTT 1560  
  
QY 1561 AATATCATTTTAAATATTAATCTTATTTGACATATGTTTAAACCAAGTAAATTTGAGTGC 1620  
DB 1561 AATATCATTTTAAATATTAATCTTATTTGACATATGTTTAAACCAAGTAAATTTGAGTGC 1620  
  
QY 1621 GGTAGTAAAACTCATTACACATTTTAAAGTAGAACGTAGTTTCAACCTTGGAGAG 1675  
DB 1621 GGTAGTAAAACTCATTACACATTTTAAAGTAGAACGTAGTTTCAACCTTGGAGAG 1675

XX ADR49368;  
 XX 18-NOV-2004 (first entry)  
 XX H7-1 transformant-associated DNA fragment #1.  
 XX  
 KW ds; plant; glyphosate-resistance; sugar beet; seed;  
 KW glyphosate-tolerant sugar beet; chloroplast transit peptide;  
 KW 5-enolpyruvyl-shikimate-3-phosphate synthase; EPSPS; H7-1 transformant;  
 KW T-DNA; CB4-EPSPS.  
 XX Unidentified.  
 XX OS  
 XX WO2004074492-A1.  
 XX  
 XX 02-SEP-2004.  
 XX 17-FEB-2004; 2004WO-EP001469.  
 XX  
 XX 20-FEB-2003; 2003EP-00003866.  
 XX 28-FEB-2003; 2003US-00376763.  
 XX (KWSS-) KWS SAAT AG.  
 XX  
 PI Kraus J, Sauerbrey E, Nehls R, Looock A, Jansen R;  
 XX WPI; 2004-652964/63.  
 XX  
 XX New sugar beet plants resistant to glyphosate, contain inserted 5-  
 PT enolpyruvyl-shikimate-3-phosphate synthase gene, which is stably  
 PT integrated and inherited.  
 XX Claim 2; SEQ ID NO 6; 79pp; German.  
 XX  
 CC This invention describes novel glyphosate-resistant Glycine max (sugar  
 CC beet) plants derived from seeds deposited as NCIMB 41158 or 41159. The  
 CC invention also describes a method for identifying glyphosate-tolerant  
 CC sugar beet and a test kit for identifying glyphosate-tolerant sugar beet,  
 CC or their cells, tissues and parts. The novel kit comprises at least one  
 CC primer pair, where one primer recognizes a foreign DNA inserted into the  
 CC genome, while the second recognises DNA within a flanking (3' or 5')  
 CC region. The plants are prepared by Agrobacterium-mediated transformation  
 CC of sugar beet, using the vector pV-BVGT08, which contains, between right  
 CC and left border sequences, a cassette containing the coding regions for  
 CC (a) chloroplast transit peptide and (b) the enzyme 5-enolpyruvyl-  
 CC shikimate-3-phosphate synthase (EPSPS) from Arabidopsis thaliana, under  
 CC control of the figwort mosaic virus promoter and the E9-3'  
 CC transcriptional terminator of Pisum sativum. One transformation event (H7  
 CC -1), which produced plants of high tolerance to glyphosate, was  
 CC characterised and found to contain an insertion of a single, intact copy  
 CC of the T-DNA, including the regulatory components, from pV-BVGT08. The  
 CC genomic sequences outside the insert region were identical with those in  
 CC a non-transformed plant and the insert was integrated stably and inherited  
 CC stably. The novel plants are highly resistant to glyphosate and retain  
 CC good properties as regards growth, yield, quality and resistance to  
 CC pathogens. This sequence represents a fragment of the H7-1 transformant  
 CC DNA found in vector pV-BVGT08.  
 XX  
 SQ Sequence 3706 BP; 943 A; 801 C; 801 G; 1161 T; 0 U; 0 Other;  
 Query Match 31.7%; Score 530.6; DB 13; Length 3706;  
 Best Local Similarity 92.9%; Pred. No. 2.8e-53;  
 Matches 592; Conservative 0; Mismatches 9; Indels 36; Gaps 2;  
 XX  
 QY 1 TGACCGAGTAAATATGAGGAGTAAACACTGTAGTTGACCAATATGCTTATCTACTA 60  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3032 TGACCGAGTAAATATGAGGAGTAAACACTGTAGTTGACCAATATGCTTATCTACTA 3091  
 QY 61 GGCAACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTCAATACAAAGTATGTC 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3092 GGCAACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTCAATACAAAGTATGTC 3151

QY 121 CTCCTGTGTTTATGACATTTATGAACTTCTCTTATGTAAATTTTCCAGAACTCTGTGAG 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3152 CTCCTGTGTTTATGACATTTATGAACTTCTCTTATGTAAATTTTCCAGAACTCTGTGAG 3211  
 QY 181 ATTCTAATCATTCGCTTTTATAATTTATAGTATTACTCATGATGTTTGTAGTATGAAAA 240  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3212 ATTCTAATCATTCGCTTTTATAATTTATAGTATTACTCATGATGTTTGTAGTATGAAAA 3271  
 QY 241 TATTTTAAATGATTTTATGATTCGCAATTCATTTGACAAATGCAACATGATCAATCGACTGC 300  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3272 TATTTTAAATGATTTTATGATTCGCAATTCATTTGACAAATGCAACATGATCAATCGACTGC 3331  
 QY 301 AGCCACTCGAGTGG-----AGGCTCATCT 325  
 DB |||||||||||  
 DB 3332 AGCCACTCGAGCGCGCCACTCGAGTGGTGGCCCGCATGCTGTAAGTTTCTCATCT 3391  
 QY 326 AAGCCCCCATTTTGGACGTGAATGTAGACACGTGCAAAATAAAGATTTCCGAATTTAGAAATA 385  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3392 AAGCCCCCATTTTGGACGTGAATGTAGACACGTGCAAAATAAAGATTTCCGAATTTAGAAATA 3451  
 QY 386 TTGTTTATGCTTTTCGCTTATAAATACGACGATCGTAATTTGTCTGTTTATCAAAATG 445  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3452 TTGTTTATGCTTTTCGCTTATAAATACGACGATCGTAATTTGTCTGTTTATCAAAATG 3511  
 QY 446 TACTTTTATGCTTTTACGCTGCGGACATCTACATTTTGAATTTGAAAAAATTTGGT 505  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3512 TACTTTTATGCTTTTACGCTGCGGACATCTACATTTTGAATTTGAAAAAATTTGGT 3570  
 QY 506 AATTACTCTTTCTTTTCCATATTTGACCATCATCTGCTGATCCATGATAGATTT 565  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3571 AATTACTCTTTCTTTTCCATATTTGACCATCATCTGCTGATCCATGATAGATTT 3630  
 QY 566 CCGGACATGAGCCATTTACAAATTCGAATATATATTA 602  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 3631 CCGGACATGAGCCATTTACAAATTCGAATATATATTA 3667  
 RESULT 3  
 ADR49367  
 ID ADR49367 standard; DNA; 3778 BP.  
 XX  
 AC ADR49367;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX Vector pV-BVGT08 H7-1 transformant insert.  
 XX  
 DE ds; plant; glyphosate-resistance; sugar beet; seed;  
 KW glyphosate-tolerant sugar beet; chloroplast transit peptide;  
 KW 5-enolpyruvyl-shikimate-3-phosphate synthase; EPSPS; H7-1 transformant;  
 KW T-DNA; pV-BVGT08.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004074492-A1.  
 XX  
 PD 02-SEP-2004.  
 XX  
 XX 17-FEB-2004; 2004WO-EP001469.  
 XX  
 XX 20-FEB-2003; 2003EP-00003866.  
 XX 28-FEB-2003; 2003US-00376763.  
 XX (KWSS-) KWS SAAT AG.  
 XX  
 XX Kraus J, Sauerbrey E, Nehls R, Looock A, Jansen R;  
 XX WPI; 2004-652964/63.  
 XX  
 XX New sugar beet plants resistant to glyphosate, contain inserted 5-  
 PT enolpyruvyl-shikimate-3-phosphate synthase gene, which is stably  
 PT integrated and inherited.  
 XX

PS Claim 14; SEQ ID NO 5; 79pp; German.

CC This invention describes novel glyphosate-resistant Glycine max (sugar  
CC beet) plants derived from seeds deposited as NCIMB 41158 or 41159. The  
CC invention also describes a method for identifying glyphosate-tolerant  
CC sugar beet and a test kit for identifying glyphosate-tolerant sugar beet,  
CC or their cells, tissues and parts. The novel kit comprises at least one  
CC primer pair, where one primer recognizes a foreign DNA inserted into the  
CC genome, while the second recognises DNA within a flanking (3' or 5')  
CC region. The plants are prepared by Agrobacterium-mediated transformation  
CC of sugar beet, using the vector pV-BVGT08, which contains, between right  
CC and left border sequences, a cassette containing the coding regions for  
CC (a) chloroplast transit peptide and (b) the enzyme 5-enolpyruvyl-  
CC shikimate-3-phosphate synthase (EPSPS) from Arabidopsis thaliana, under  
CC control of the figwort mosaic virus promoter and the E9-3'  
CC transcriptional terminator of Pisum sativum. One transformation event (H7  
CC -1), which produced plants of high tolerance to glyphosate, was  
CC characterised and found to contain an insertion of a single, intact copy  
CC of the T-DNA, including the regulatory components, from pV-BVGT08. The  
CC genomic sequences outside the insert region were identical with those in  
CC a non-transformed plant and the insert was integrated stably and inherited  
CC stably. The novel plants are highly resistant to glyphosate and retain  
CC good properties as regards growth, yield, quality and resistance to  
CC pathogens. This sequence represents the vector pV-GVGT08 H7-1  
CC transformant insert.

XX SQ Sequence 3778 BP; 958 A; 822 C; 823 G; 1175 T; 0 U; 0 Other;

Query Match 31.7%; Score 530.6; DB 13; Length 3778;  
Best Local Similarity 92.9%; Pred. No. 2.8e-53;  
Matches 592; Conservative 0; Mismatches 9; Indels 36; Gaps 2;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGTACCATATGCTTATTCACATA 60  
DB 3077 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGTACCATATGCTTATTCACATA 3136  
QY 61 GCGACAAATATATTTTCAGACCTAGAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120  
DB 3137 GCGACAAATATATTTTCAGACCTAGAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 3196  
QY 121 CTCCTGTGTTTATGACATTTATGAATTTCTTATGTAATTTTCCAGAAATCCTTGTCTCAG 180  
DB 3197 CTCCTGTGTTTATGACATTTATGAATTTCTTATGTAATTTTCCAGAAATCCTTGTCTCAG 3256  
QY 181 ATCTAATCATGCTTTTAAAT 240  
DB 3257 ATCTAATCATGCTTTTAAAT 3316  
QY 241 TATTTTAAATGATTTTATGACTTGCCTTATGCTTATGCTTATGCTTATGCTTATGCTTATG 300  
DB 3317 TATTTTAAATGATTTTATGACTTGCCTTATGCTTATGCTTATGCTTATGCTTATGCTTATG 3376  
QY 301 AGCCACTCGAGTGG-----AGGCCTCATCT 325  
DB 3377 AGCCACTCGAGCGGCGCCACTCGAGTGGTGGCCGCGATCGATCGTGAAGTTTCTCATCT 3436  
QY 326 AAGCCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATAA 385  
DB 3437 AAGCCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATAA 3496  
QY 386 TTTGTTTATGCTTTTGCCTTAAATATACGAGATCGTAAATTTGCTTTTATCAAAATG 445  
DB 3497 TTTGTTTATGCTTTTGCCTTAAATATACGAGATCGTAAATTTGCTTTTATCAAAATG 3556  
QY 446 TACTTTTCATTTTATATAACGCTGCGGACATCTACATTTTTCGAATTTGAAAAAATTTGCT 505  
DB 3557 TACTTTTCATTTTATATAACGCTGCGGACATCTACATTTTTCGAATTTGAAAAAATTTGCT 3615  
QY 506 AATTAATCTTTCTTTTCTCCATATTTAGCCATCATCTACTGCTGATCCATGTAGATTT 565  
DB 3616 AATTAATCTTTCTTTTCTCCATATTTAGCCATCATCTACTGCTGATCCATGTAGATTT 3675  
QY 566 CCCGGACATGAAGCCATTTTACAAATGAATATATATTA 602

DB 3676 CCCGGACATGAAGCCATTTTACAAATGAATATATCTTA 3712

RESULT 4

ABB71496/c

ID AEB71496 standard; DNA; 7794 BP.

XX AC AEB71496;

XX 20-OCT-2005 (first entry)

DE A. tumefaciens transformation vector DNA SEQ ID NO:2.

XX vector; recombinant DNA; transgenic plant; ds.

XX Agrobacterium tumefaciens.

OS Pisum sativum.

XX Zea mays.

Key Location/Qualifiers

FT misc\_feature 1..357

FT /tag= a

FT /note= "A. tumefaciens right border"

FT misc\_feature 376..1774

FT /tag= b

FT /note= "Rice actin promoter and intron"

FT CDS 1784..2011

FT /tag= c

FT /product= "A. tumefaciens EPSPS chloroplast transit

FT peptide"

FT CDS 2012..3379

FT /tag= d

FT /product= "A. tumefaciens aroA"

FT misc\_feature 3395..3647

FT /tag= e

FT /note= "A. tumefaciens NOS terminator"

FT misc\_feature 3479..4391

FT /tag= f

FT /note= "Pisum sativum RbcS2 terminator"

FT misc\_feature 4398..4748

FT /tag= g

FT /note= "Zea mays alpha zein gene Z198 fragment"

FT misc\_feature 4755..5043

FT /tag= h

FT /note= "Zea mays alpha zein gene Z22s fragment"

FT misc\_feature 5050..5835

FT /tag= i

FT /note= "Zea mays alpha zein gene Z22asL fragment"

FT misc\_feature 5842..6192

FT /tag= j

FT /note= "Zea mays alpha zein gene Z19as fragment"

FT misc\_feature 6204..7305

FT /tag= k

FT /note= "Zea mays gamma zein gene Z27 promoter"

FT misc\_feature 7353..7794

FT /tag= l

XX /note= "A. tumefaciens left border"

PN US2005176670-A1.

XX 11-AUG-2005.

XX 10-FEB-2005; 2005US-00057062.

XX 10-FEB-2004; 2004US-0543157P.

XX 10-FEB-2004; 2004US-0543187P.

XX 11-AUG-2004; 2004US-0600859P.

XX (HUAN/) HUANG S.

XX (MALV/) MALVAR T M.

XX (LUET/) LUETHY M H.

XX





DT 20-MAR-2003 (revised)  
XX 26-JUL-1999 (first entry)  
XX  
DE Sugar beet T-DNA containing cp4/epsps #2.  
XX  
XX Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;  
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;  
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.  
XX  
XX Beta vulgaris.  
OS  
XX WO9923232-A1.  
XX  
XX 14-MAY-1999.  
XX  
XX 29-OCT-1998; 98WO-EP006859.  
XX  
XX 31-OCT-1997; 97US-00962467.  
XX  
XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
XX Mannerloef M, Tenning PP, Steen P;  
PI  
XX WPI; 1999-313347/26.  
XX  
XX Glyphosate resistant transgenic sugar beet plants.  
XX  
XX Claim 15; Page 36-41; 55pp; English.  
XX  
XX This invention describes a novel sugar beet plant, including its  
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated  
CC transformation with a gene allowing expression of cp4/epsps in plants,  
CC where the plant lacks both right and left T-DNA border sequences. The  
CC transgenic sugar beet plants of the invention are capable of tolerating  
CC herbicide treatment with glyphosate (also known as N-phosphonomethyl-  
CC glycine) as the active ingredient, e.g. Roundup. (Updated on 20-MAR-2003  
CC to correct PR field.)  
XX  
SQ Sequence 8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 U; 0 Other;  
Query Match 18.5%; Score 310; DB 2; Length 8418;  
Best Local Similarity 100.0%; Pred. No. 7.7e-28;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 60  
Db 2687 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 2746  
QY 61 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTGTACTGCAATACAGTATGTC 120  
Db 2747 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTGTACTGCAATACAGTATGTC 2806  
QY 121 CTCCTGTGTTTTAGACATTTATGCACTTCCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180  
Db 2807 CTCCTGTGTTTTAGACATTTATGCACTTCCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 2866  
QY 181 ATTCCTAATCATTCCTTTTAAATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 240  
Db 2867 ATTCCTAATCATTCCTTTTAAATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 2926  
QY 241 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGCAATGCAACATGCAATCGACTGCG 300  
Db 2927 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGCAATGCAACATGCAATCGACTGCG 2986  
QY 301 AGCCACTCGA 310  
Db 2987 AGCCACTCGA 2996

ID AAX57308 standard; DNA; 8798 BP.  
XX  
AC AAX57308;  
XX  
XX 20-MAR-2003 (revised)  
DT 26-JUL-1999 (first entry)  
XX  
DE Sugar beet T-DNA containing cp4/epsps.  
XX  
XX Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;  
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;  
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.  
XX  
XX Beta vulgaris.  
OS  
XX WO9923232-A1.  
XX  
XX 14-MAY-1999.  
XX  
XX 29-OCT-1998; 98WO-EP006859.  
XX  
XX 31-OCT-1997; 97US-00962467.  
XX  
XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
XX Mannerloef M, Tenning PP, Steen P;  
PI  
XX WPI; 1999-313347/26.  
XX  
XX Glyphosate resistant transgenic sugar beet plants.  
XX  
XX Claim 11; Page 31-36; 55pp; English.  
XX  
XX This invention describes a novel sugar beet plant, including its  
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase  
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated  
CC transformation with a gene allowing expression of cp4/epsps in plants,  
CC where the plant lacks both right and left T-DNA border sequences. The  
CC transgenic sugar beet plants of the invention are capable of tolerating  
CC herbicide treatment with glyphosate (also known as N-phosphonomethyl-  
CC glycine) as the active ingredient, e.g. Roundup. (Updated on 20-MAR-2003  
CC to correct PR field.)  
XX  
SQ Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 U; 0 Other;  
Query Match 18.5%; Score 310; DB 2; Length 8798;  
Best Local Similarity 100.0%; Pred. No. 7.7e-28;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 60  
Db 2797 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 2856  
QY 61 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTGTACTGCAATACAGTATGTC 120  
Db 2857 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTGTACTGCAATACAGTATGTC 2916  
QY 121 CTCCTGTGTTTTAGACATTTATGCACTTCCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180  
Db 2917 CTCCTGTGTTTTAGACATTTATGCACTTCCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 2976  
QY 181 ATTCCTAATCATTCCTTTTAAATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 240  
Db 2977 ATTCCTAATCATTCCTTTTAAATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 3036  
QY 241 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGCAATGCAACATGCAATCGACTGCG 300  
Db 3037 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGCAATGCAACATGCAATCGACTGCG 3096  
QY 301 AGCCACTCGA 310  
Db 3097 AGCCACTCGA 3106

RESULT 8  
 ID ABS54336 standard; DNA; 10846 BP.  
 XX  
 AC ABS54336;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE E. coli fda gene, plant transformation vector pMON17524.  
 XX  
 KW Fructose-1,6-bisphosphate aldolase; FDA; triosephosphate;  
 KW plant chloroplast; starch synthesis; cytosol; sucrose synthesis;  
 KW carbon assimilation; carbon storage; carbon export; transgenic; potato;  
 KW food production; French fry; photosynthesis; plant yield; plant growth;  
 KW potato tuber; blanch; dry; par-fry; cyclic; circular; ds.  
 XX  
 OS Escherichia coli.  
 OS Arabidopsis sp.  
 OS Figwort mosaic virus.  
 OS Synthetic.  
 XX  
 PN US6441277-B1.  
 XX  
 PD 27-AUG-2002.  
 XX  
 PF 16-JUN-1998; 98US-00098219.  
 XX  
 PR 17-JUN-1997; 97US-0049955P.  
 XX  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX  
 PI Barry GF, Cheikh N, Kishore GM;  
 XX  
 DR WPI; 2002-711539/77.  
 XX  
 PT Novel recombinant, DNA molecule for producing genetically transformed  
 PT plants having elevated carbon assimilation, has promoter functional in  
 PT plant cells, and DNA sequence encoding fructose-1,6-bisphosphate  
 PT aldolase.  
 XX  
 PS Example 2; Col 35-44; 39pp; English.  
 XX  
 CC The present invention relates to a recombinant, double-stranded DNA  
 CC vector, comprising a promoter functional in plant cells, and a DNA  
 CC sequence from a prokaryotic organism (e.g. Escherichia coli) coding for  
 CC fructose-1,6-bisphosphate aldolase (FDA), where the DNA sequence is  
 CC operatively linked to the promoter in the sense orientation. FDA  
 CC catalyses the conversion of triosephosphate into fructose-1,6  
 CC bisphosphate in plant chloroplasts (starch synthesis) and in the cytosol  
 CC (sucrose synthesis). The recombinant DNA vector of the invention is  
 CC useful for producing genetically transformed plants that have elevated  
 CC carbon assimilation, storage, export and improved uniformity of solids  
 CC (e.g. in transgenic potatoes expressing fda). The vector of the invention  
 CC is particularly useful in the commercial production of foods derived from  
 CC potatoes which are useful for producing French fries. The transgenic  
 CC plants exhibit increased photosynthesis rate, increased plant yield,  
 CC increased growth rate and increased solids uniformity compared with  
 CC plants that do not contain the recombinant DNA vector. The recombinant  
 CC DNA vector provides higher quality, more uniform potato tuber regions,  
 CC and therefore french fries. This results in a higher throughput in the  
 CC French fry processing plant due to lower processing times, and processor  
 CC cost savings due to lower energy input required for lower blanch, dry,  
 CC and par-fry times. The present sequence represents a plant transformation  
 CC vector containing the E. coli fda gene  
 XX  
 SQ Sequence 10846 BP; 2669 A; 2760 C; 2681 G; 2736 T; 0 U; 0 Other;  
 Query Match 18.5%; Score 310; DB 6; Length 10846;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-28;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGAGTAAACACTTGTAGTTGTACCAATTATGCTTATTCCTA 60  
 DB |||||  
 2059 TGACCGAAGTTAATATGAGAGTAAACACTTGTAGTTGTACCAATTATGCTTATTCCTA 2118  
 QY 61 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGCTTACTGAATACAACTATGTC 120  
 DB |||||  
 2119 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGCTTACTGAATACAACTATGTC 2178  
 QY 121 CTCTTGTTGTTTAGACATTTATGAACCTTCTCTTATGTATTTTCCAGAAATCCTTGTGTCAG 180  
 DB |||||  
 2179 CTCTTGTTGTTTAGACATTTATGAACCTTCTCTTATGTATTTTCCAGAAATCCTTGTGTCAG 2238  
 QY 181 ATTCTAATCATCTGCTTTAATTAATTATAGTTATATCTATGATTTGTAGTGATGAAAA 240  
 DB |||||  
 2239 ATTCTAATCATCTGCTTTAATTAATTATAGTTATATCTATGATTTGTAGTGATGAAAA 2298  
 QY 241 TATTTTAAATGATTTTATGACTTCCCAATTCGATTCGACCAATGCAATCATCAATCGACCTGC 300  
 DB |||||  
 2299 TATTTTAAATGATTTTATGACTTCCCAATTCGATTCGACCAATGCAATCATCAATCGACCTGC 2358  
 QY 301 AGCCACTCGA 310  
 DB |||||  
 2359 AGCCACTCGA 2368  
 RESULT 9  
 AAX08923  
 ID AAX08923 standard; DNA; 10847 BP.  
 XX  
 AC AAX08923;  
 XX  
 DT 27-APR-1999 (first entry)  
 XX  
 DE Vector comprising fructose-1,6-bisphosphate aldolase (FDA) gene.  
 XX  
 KW Fructose-1,6-bisphosphate aldolase; FDA; carbon assimilation; starch;  
 KW sucrose; crop; yield; growth; transgenic plant; potato; photosynthesis;  
 KW ds.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9858069-A1.  
 XX  
 PD 23-DEC-1998.  
 XX  
 PF 16-JUN-1998; 98WO-US012447.  
 XX  
 PR 17-JUN-1997; 97US-0049955P.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Barry GF, Cheikh N, Kishore GM;  
 XX  
 DR WPI; 1999-095343/08.  
 XX  
 PT Use of fructose-1,6-trisphosphate aldolase DNA - useful for, e.g.  
 PT producing transgenic plants with increased photosynthesis rates,  
 PT increased yields, increased growth rates and improved solids uniformity.  
 XX  
 PS Example 2; Page 51-54; 75pp; English.  
 XX  
 CC Fructose-1,6-bisphosphate aldolase (FDA) catalyses the reversible  
 CC reaction converting triosephosphate into fructose-1,6-bisphosphate  
 CC aldolase. By inserting the FDA gene into expression vectors and inserting  
 CC these vectors into the chloroplasts of plant cells, increased starch  
 CC production can be achieved. Increasing the expression of the FDA enzyme  
 CC in the chloroplast increases carbon assimilation and results in an  
 CC increase in chloroplast starch production. This increase in carbon  
 CC assimilation is a desirable trait in crop plants and leads to increased  
 CC plant growth, storage ability, yield, vigour, and stress tolerance.  
 CC Increasing FDA expression in the cytosol of photosynthetic cells leads to  
 CC an increase in sucrose production. The transgenic plants containing the  
 CC recombinant DNA can have increased photosynthesis rates, increased

```
CC yields, increased growth rates and improved solids uniformity compared
CC with plants that do not contain the recombinant DNA molecule. Vectors
CC containing the recombinant FDA gene are used particularly for improving
CC potato products. This sequence describes the vector designated pMON17524
CC which comprises the E.coli FDA gene fused to the Arabidopsis small
CC subunit CTPI. This vector was used for tobacco plant transformation
XX
SQ Sequence 10847 BP; 2669 A; 2760 C; 2681 G; 2736 T; 0 U; 1 Other;
Query Match 18.5%; Score 310; DB 2; Length 10847;
Best Local Similarity 100.0%; Pred. No. 7.4e-28;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGACCGAAGTTAATATGAGGAGTAACACACTTGTAGTTGACCAATTCCTTATTCACCTA 60
DB 2059 TGACCGAAGTTAATATGAGGAGTAACACACTTGTAGTTGACCAATTCCTTATTCACCTA 2118
QY 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120
DB 2119 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 2178
QY 121 CTCTGTGTTTTAGACATTTATGAACCTTCCTTTATGTATATTTCCAGAAATCCTTGTGCAG 180
DB 2179 CTCTGTGTTTTAGACATTTATGAACCTTCCTTTATGTATATTTCCAGAAATCCTTGTGCAG 2238
QY 181 ATTCTAATCATTCGCTTTATATATATAGTTTACTCATGGATTTGTAGTTGAGTATGAAA 240
DB 2239 ATTCTAATCATTCGCTTTATATATATAGTTTACTCATGGATTTGTAGTTGAGTATGAAA 2298
QY 241 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCAATGCAATCGACTGC 300
DB 2299 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCAATGCAATCGACTGC 2358
QY 301 AGCCACTCGA 310
DB 2359 AGCCACTCGA 2368
RESULT 10
AA08924
ID AA08924 standard; DNA; 10900 BP.
XX
AC AA08924;
XX
DT 27-APR-1999 (first entry)
XX
DE Vector comprising fructose-1,6-bisphosphate aldolase (FDA) gene.
XX
KW Fructose-1,6-bisphosphate aldolase; FDA; carbon assimilation; starch;
KW sucrose; crop; yield; growth; transgenic plant; potato; photosynthesis;
KW db.
XX
OS Synthetic.
XX
XX WO9858069-A1.
XX
PD 23-DEC-1998.
XX
PF 16-JUN-1998; 98WO-US012447.
XX
PR 17-JUN-1997; 97US-0049955P.
XX
PA (MONS ) MONSANTO CO.
XX
PI Barry GF, Cheikh N, Kishore GM;
XX
XX WPI; 1999-095343/08.
XX
PT Use of fructose-1,6-triphosphate aldolase DNA - useful for, e.g.
PT producing transgenic plants with increased photosynthesis rates,
PT increased yields, increased growth rates and improved solids uniformity.
XX
PS Example 2; Page 55-58; 75pp; English.
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XX Fructose-1,6-bisphosphate aldolase (FDA) catalyses the reversible
CC reaction converting triosephosphate into fructose-1,6-bisphosphate
CC aldolase. By inserting the FDA gene into expression vectors and inserting
CC these vectors into the chloroplasts of plant cells, increased starch
CC production can be achieved. Increasing the expression of the FDA enzyme
CC in the chloroplast increases carbon assimilation and results in an
CC increase in chloroplast starch production. This increase in carbon
CC assimilation is a desirable trait in crop plants and leads to increased
CC plant growth, storage ability, yield, vigour, and stress tolerance.
CC Increasing FDA expression in the cytosol of photosynthetic cells leads to
CC an increase in sucrose production. The transgenic plants containing the
CC recombinant DNA can have increased photosynthesis rates, increased
CC yields, increased growth rates and improved solids uniformity compared
CC with plants that do not contain the recombinant DNA molecule. Vectors
CC containing the recombinant FDA gene are used particularly for improving
CC potato products. This sequence describes the vector designated pMON17542
CC which comprises the E.coli FDA gene fused to the Arabidopsis small
CC subunit CTPI and the Arabidopsis EPSPS (CP2) transit peptide. This
CC vector was used for tobacco plant transformation
XX
SQ Sequence 10900 BP; 2691 A; 2750 C; 2694 G; 2764 T; 0 U; 1 Other;
Query Match 18.5%; Score 310; DB 2; Length 10900;
Best Local Similarity 100.0%; Pred. No. 7.4e-28;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGACCGAAGTTAATATGAGGAGTAACACACTTGTAGTTGACCAATTCCTTATTCACCTA 60
DB 2059 TGACCGAAGTTAATATGAGGAGTAACACACTTGTAGTTGACCAATTCCTTATTCACCTA 2118
QY 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120
DB 2119 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 2178
QY 121 CTCTGTGTTTTAGACATTTATGAACCTTCCTTTATGTATATTTCCAGAAATCCTTGTGCAG 180
DB 2179 CTCTGTGTTTTAGACATTTATGAACCTTCCTTTATGTATATTTCCAGAAATCCTTGTGCAG 2238
QY 181 ATTCTAATCATTCGCTTTTATAATATATAGTTTACTCATGGATTTGTAGTTGAGTATGAAA 240
DB 2239 ATTCTAATCATTCGCTTTTATAATATATAGTTTACTCATGGATTTGTAGTTGAGTATGAAA 2298
QY 241 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCAATGCAATCGACTGC 300
DB 2299 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCAATGCAATCGACTGC 2358
QY 301 AGCCACTCGA 310
DB 2359 AGCCACTCGA 2368
RESULT 11
ABS54337
ID ABS54337 standard; DNA; 10900 BP.
XX
AC ABS54337;
XX
DT 12-DEC-2002 (first entry)
XX
DE E. coli fda gene, plant transformation vector pMON17542.
XX
KW Fructose-1,6-bisphosphate aldolase; FDA; triosephosphate;
KW plant chloroplast; starch synthesis; cytosol; sucrose synthesis;
KW carbon assimilation; carbon storage; carbon export; transgenic; potato;
KW food production; French fry; photosynthesis; plant yield; plant growth;
KW potato tuber; blanch; dry; par-fry; cyclic; circular; ds.
XX
OS Escherichia coli.
OS Arabidopsis sp.
OS Figwort mosaic virus.
OS Synthetic.
XX
```

PN US6441277-B1.  
 XX 27-AUG-2002.  
 XX 16-JUN-1998; 98US-00098219.  
 XX 17-JUN-1997; 97US-0049995P.  
 XX (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX Barry GF, Cheikh N, Kishore GM;  
 XX WPI; 2002-711539/77.  
 XX Novel recombinant, DNA molecule for producing genetically transformed  
 XX plants having elevated carbon assimilation, has promoter functional in  
 XX plant cells, and DNA sequence encoding fructose-1,6-bisphosphate  
 XX aldolase.  
 XX  
 XX Example 2; Col 45-54; 39pp; English.  
 XX  
 XX The present invention relates to a recombinant, double-stranded DNA  
 XX vector, comprising a promoter functional in plant cells, and a DNA  
 XX sequence from a prokaryotic organism (e.g. *Escherichia coli*) coding for  
 XX fructose-1,6-bisphosphate aldolase (fda), where the DNA sequence is  
 XX operatively linked to the promoter in the sense orientation. fda  
 XX catalyses the conversion of triosephosphate into fructose-1,6  
 XX bisphosphate in plant chloroplasts (starch synthesis) and in the cytosol  
 XX (sucrose synthesis). The recombinant DNA vector of the invention is  
 XX useful for producing genetically transformed plants that have elevated  
 XX carbon assimilation, storage, export and improved uniformity of solids  
 XX (e.g. in transgenic potatoes expressing fda). The vector of the invention  
 XX is particularly useful in the commercial production of foods derived from  
 XX potatoes which are useful for producing French fries. The transgenic  
 XX plants exhibit increased photosynthesis rate, increased plant yield,  
 XX increased growth rate and increased solids uniformity compared with  
 XX plants that do not contain the recombinant DNA vector. The recombinant  
 XX DNA vector provides higher quality, more uniform potato tuber regions,  
 XX and therefore french fries. This results in a higher throughput in the  
 XX french fry processing plant due to lower processing times, and processor  
 XX cost savings due to lower energy input required for lower blanch, dry,  
 XX and par-fry times. The present sequence represents a plant transformation  
 XX vector containing the *E. coli* fda gene  
 XX  
 XX Sequence 10900 BP; 2691 A; 2749 C; 2695 G; 2765 T; 0 U; 0 Other;  
 PS  
 PS Query Match 18.5%; Score 310; DB 6; Length 10900;  
 PS Best Local Similarity 100.0%; Pred. No. 7.4e-28;  
 PS Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTGTGTAGTGTACCAATTATGCTTATTCACCTA 60  
 Db |||||||  
 QY 2059 TGACCGAAGTTAATATGAGGAGTAAACACTGTGTAGTGTACCAATTATGCTTATTCACCTA 2118  
 Db |||||||  
 QY 61 GGCAACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120  
 Db |||||||  
 QY 2119 GGCAACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 2178  
 Db |||||||  
 QY 121 CTCCTGTGTTTTCAGACATTTATGAACTTCTTATGTAATTTTCCAGAAATCCTGTGTCAG 180  
 Db |||||||  
 QY 2179 CTCCTGTGTTTTCAGACATTTATGAACTTCTTATGTAATTTTCCAGAAATCCTGTGTCAG 2238  
 Db |||||||  
 QY 181 ATTCCTAATCATGCTTTTATATATATAGTATATCTACTCATGGATTTGTAGTTCAGTATGAAA 240  
 Db |||||||  
 QY 2239 ATTCCTAATCATGCTTTTATATATATAGTATATCTACTCATGGATTTGTAGTTCAGTATGAAA 2298  
 Db |||||||  
 QY 241 TATTTTAAATGCAATTTTATGCACTTGCCAAATTCATTCGACCAATGCAATGCAATGCAATGCA 300  
 Db |||||||  
 QY 2299 TATTTTAAATGCAATTTTATGCACTTGCCAAATTCATTCGACCAATGCAATGCAATGCA 2358  
 Db |||||||  
 QY 301 AGCCACTCGA 310  
 Db |||||||  
 QY 2359 AGCCACTCGA 2368  
 Db |||||||

## RESULT 12

ADQ13598  
 ID ADQ13598 standard; DNA; 11606 BP.  
 XX  
 AC ADQ13598;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Plasmid pLBS107 expressing mutant ethylene receptor etr1-1.  
 XX  
 KW Cotton; ethylene receptor; ds; ethylene insensitivity;  
 KW abscission zone tissue; plant; transgenic; flower drop; fruit drop;  
 KW leaf drop; EIN; ethylene insensitive; EIL; ethylene insensitive-like;  
 KW chitinase; cellulase; polygalacturonase; pLBS107; cyclic; circular.  
 XX  
 OS *Gossypium hirsutum*.  
 OS *Arabidopsis thaliana*.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1674..3890  
 FT /\*cag= a  
 FT /product= "mutant ethylene receptor etr-1"  
 XX  
 PN US2004128719-A1.  
 XX  
 PD 01-JUL-2004.  
 XX  
 XX 23-JUN-2003; 2003US-00602475.  
 PF  
 PF 21-JUN-2002; 2002US-0390385P.  
 PR  
 XX (KLEE/) KLEE H J.  
 PA (LASH/) LASHBROOK C.  
 PA (SHRO/) SHRODE L.  
 XX  
 XX Klee HJ, Lashbrook C, Shrode L;  
 XX WPI; 2004-533137/51.  
 XX  
 XX New polynucleotide encoding a mutant plant ethylene receptor protein,  
 XX useful in decreasing flower, fruit, or leaf drop in a plant upon exposure  
 XX to ethylene.  
 XX  
 XX Example 2; SEQ ID NO 9; 59pp; English.  
 PS  
 XX The invention relates to a new polynucleotide comprising (i) a nucleotide  
 XX sequence encoding a mutant plant ethylene receptor protein, or its  
 XX fragment, which exhibits ethylene insensitivity, and (ii) a regulatory  
 XX nucleotide sequence operably linked to the protein encoding nucleotide,  
 XX sequence, where the regulatory nucleotide sequence promotes transcription  
 XX of the protein encoding nucleotide sequence in cells that comprises  
 XX abscission zone tissue of a plant. Also included are a cell transformed  
 XX with the polynucleotide, a plant, plant tissue, or a plant cell  
 XX transformed with or bred to contain the polynucleotide and a method for  
 XX decreasing flower, fruit, or leaf drop in a plant upon exposure to  
 XX ethylene, comprises introducing the polynucleotide into a plant. The  
 XX polynucleotide preferably comprises a nucleotide sequence encoding a  
 XX plant EIN (ethylene insensitive), EIL (ethylene insensitive-like) gene  
 XX product or a mutant ethylene receptor protein is (etr1, etr2, ers1, ers2,  
 XX or ein4 mutant receptors). The regulatory nucleotide sequence comprises a  
 XX promoter sequence from a plant chitinase, cellulase, or polygalacturonase  
 XX gene. The polynucleotide, protein, and method are useful in decreasing  
 XX flower, fruit, or leaf drop in a plant upon exposure to ethylene. The  
 XX present sequence represents plasmid pLBS107 expressing mutant ethylene  
 XX receptor etr1-1 from the cotton chitinase promoter.  
 XX  
 SQ Sequence 11606 BP; 3014 A; 2696 C; 2782 G; 3113 T; 0 U; 1 Other;  
 Query Match 18.5%; Score 310; DB 12; Length 11606;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-28;



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PF 07-MAY-2002; 2002WO-US014481.
XX
PR 07-MAY-2001; 2001US-0289315P.
XX
PA (POLS/) POLSTON J E.
PA (HIEB/) HIEBERT E.
XX
PI Polston JE, Hiebert E.
XX
XX WPI; 2003-120538/11.
XX
XX Providing resistance to infection by a tomato yellow leaf curl virus in a
PT plant or plant tissue comprises transforming the plant or plant tissue
PT with a polynucleotide.
XX
XX Disclosure; Page 40-41; 41pp; English.
XX
XX The present sequence is the nucleotide sequence of an expression cassette
CC in pKYLX71:35S2. The promoter in this plasmid is a 35S promoter modified
CC by a duplicated enhancer region. The invention provides a means for
CC producing virus resistance in tomato and other crops to infection by
CC tomato yellow leaf curl virus-Israel (TYLCV-Is). A claimed method of
CC providing resistance in a plant involves transforming the plant with a
CC polynucleotide comprising a fragment of a TYLCV Rep gene, a
CC polynucleotide antisense to the truncated Rep gene, or a polynucleotide
CC that hybridizes to the truncated Rep gene or antisense sequence. The
CC plant is selected from statice, petunia, lisianthus, tomatillo, and
CC especially tomato or tobacco, and transformation is performed by
CC agroinfection, biolistic targetting, electroporation or direct gene
CC injection. (Updated on 27-OCT-2003 to standardise OS field)
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XX Sequence 1998 BP; 625 A; 411 C; 408 G; 554 T; 0 U; 0 Other;
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XX Query Match 17.6%; Score 295; DB 8; Length 1998;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-26;
XX Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTTGCTTATTCACCTA 60
DB 1703 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTTGCTTATTCACCTA 1762
QY 61 GGCAACAAATATATTTTACAGACTAGAAAAGCTGCAAAATGTTACTGAATCAAGTATGTC 120
DB 1763 GGCAACAAATATATTTTACAGACTAGAAAAGCTGCAAAATGTTACTGAATCAAGTATGTC 1822
QY 121 CTCCTGTGTTTATAGACATTTATCACTTTCCTTTATGTAATTTTCCAGATCCTTCTCAG 180
DB 1823 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGATCCTTCTCAG 1882
QY 181 ATTCTAATCATTTGCTTTTATATATATATATATATATATATATATATATATATATATAT 240
DB 1883 ATTCTAATCATTTGCTTTTATATATATATATATATATATATATATATATATATATATAT 1942
QY 241 TATTTTAAATGATTTTATGATCTGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 295
DB 1943 TATTTTAAATGATTTTATGATCTGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 1997
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RESULT 15
ABV75876
ID ABV75876 standard; DNA; 12304 BP.
XX
XX ABV75876;
XX
XX 05-FEB-2003 (first entry)
XX
XX Luciferase expression vector ACT-OM-LUC.
XX
XX Vector; ACT-OM-LUC; transgenic plant; bioluminescence; luminescence;
XX firefly; luciferase; enzyme; plant; gene; ds.
XX
XX Photinus; sp.
XX
XX Tobacco mosaic virus.
XX
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OS Unidentified.
OS Chimeric.
XX
XX Key Location/Qualifiers
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XX enhancer 6..1145
XX /tag= b
XX /note= "actin 2 enhancer and promoter"
XX enhancer 1167..1235
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XX enhancer"
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XX WO200281647-A2.
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XX 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US011116.
XX
XX 06-APR-2001; 2001US-0282094P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Kay SA, Kuhlmann T, Lerner RA;
XX
XX WPI; 2003-058526/05.
XX
XX Novel genetically modified plant cell, useful as research tool, comprises
XX a heterologous nucleotide sequence encoding a bioluminescent polypeptide
XX expressed in an amount sufficient to produce visible light.
XX
XX Claim 21; Page 90-96; 96pp; English.
XX
XX The present sequence is that of luciferase expression vector ACT-OM-LUC
XX comprising an expression construct composed of an actin 2 regulatory
XX element comprising an enhancer and promoter, a tobacco mosaic virus omega
XX translational enhancer, a nucleotide sequence encoding luciferase, and an
XX Rbcs E9 polyA region. Claimed vectors, including ACT-OM-LUC, can be used
XX to transform a plant cell such that the cell expresses luciferase in an
XX amount sufficient to produce at least 750,000 photons of visible light/sq
XX mm/second. Also claimed are visibly bioluminescent transgenic plants that
XX contain the genetically modified plant cell. The transgenic plant may be
XX a monocot or dicot, including an angiosperm, cereal, legume, oilseed
XX plant or hardwood tree, or an ornamental plant such as petunia or
XX carnation (all claimed). The transgenic plants are useful as research
XX tools and have ornamental value
XX
XX Sequence 12304 BP; 2928 A; 3115 C; 3142 G; 3119 T; 0 U; 0 Other;
XX
XX Query Match 17.3%; Score 289; DB 8; Length 12304;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-25;
XX Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTTGCTTATTCACCTA 60
DB 3280 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTTGCTTATTCACCTA 3339
QY 61 GGCAACAAATATATTTTACAGACTAGAAAAGCTGCAAAATGTTACTGAATCAAGTATGTC 120
DB 3340 GGCAACAAATATATTTTACAGACTAGAAAAGCTGCAAAATGTTACTGAATCAAGTATGTC 3399
QY 121 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGATCCTTCTCAG 180
DB 3400 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGATCCTTCTCAG 3459
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Qy 181 ATTCTAATCATTCGCTTTTATAATTATAGTTTATCTCATGGATTGTAGTTGAGTATGAAAA 240  
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Db 3460 ATTCTAATCATTCGCTTTTATAATTATAGTTTATCTCATGGATTGTAGTTGAGTATGAAAA 3519  
|||

Qy 241 TATTTTTTAATGCATTTTATGACTTGCCCAATTGATTGACACACATGCATC 289  
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Db 3520 TATTTTTTAATGCATTTTATGACTTGCCCAATTGATTGACACACATGCATC 3568  
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Job time : 1110.43 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:33:28 ; Search time 7670.01 Seconds  
(without alignments)  
10217.511 Million cell updates/sec

Title: US-10-541-346-4  
Perfect score: 1675  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	280	16.7	865	10	AJ517094 Arabidops
C 3	280	16.7	956	10	ATH516972 Arabidops
4	277.4	16.6	1146	10	AJ517056 Arabidops
C 5	258.4	15.4	863	10	ATH517085 Arabidops
6	256	15.3	796	10	AJ517067 Arabidops
7	256	15.3	1601	10	ATH517045 Arabidops
C 8	221.2	13.2	808	10	ATH517113 Arabidops
C 9	218.4	13.0	970	10	ATH516966 Arabidops
C 10	201	12.0	975	10	ATH516980 Arabidops
11	169.8	10.1	1896	10	CG753083 Arabidops
12	169	10.1	1313	7	CK997149 Arabidops
C 13	164.2	9.8	1896	10	CG753083 Arabidops
C 14	162.6	9.7	1227	10	AG430010 Mus muscu
C 15	162.2	9.7	820	10	ATH517144 Arabidops
16	162.2	9.7	1277	9	CC253231 Arabidops
17	161.2	9.6	1238	1	AJ925855 Arabidops
C 18	160.8	9.6	1359	8	DN685273 Arabidops
C 19	160.6	9.6	1202	9	CC262481 Arabidops
C 20	156.2	9.3	1542	10	AG386981 Arabidops
C 21	155.2	9.3	1392	10	CG757503 Arabidops
C 22	154	9.2	1391	10	CG754863 Arabidops

23 153.4 9.2 1189 1 AJ925925  
C 24 153 9.1 1313 7 CK997149  
C 25 152.8 9.1 1592 10 CG750135  
C 26 152.6 9.1 1211 10 AG349657 Mus muscu  
C 27 152 9.1 817 10 ATH516963 Arabidops  
28 151.6 9.1 1101 10 CNS0021J Arabidops  
29 151.6 9.1 1325 10 CG952344 Arabidops  
C 30 151.4 9.0 1268 10 AG347098 Arabidops  
C 31 151.2 9.0 1242 10 CL068807 Arabidops  
32 150.8 9.0 1101 10 CNS008VL Arabidops  
C 33 150.4 9.0 1489 10 AG350139 Arabidops  
C 34 150 9.0 1378 10 AG350209 Arabidops  
C 35 149.8 8.9 1489 10 AG350139 Arabidops  
36 149 8.9 976 10 CG949642 Arabidops  
C 37 149 8.9 1539 10 AG340947 Arabidops  
38 148.4 8.9 991 10 CL139092 Arabidops  
39 148.4 8.9 1608 10 CL118721 Arabidops  
40 148.2 8.8 1092 1 AJ927993 Arabidops  
C 41 147.2 8.8 1254 10 AG349719 Arabidops  
42 146.8 8.8 1359 8 DN685273 Arabidops  
43 146.4 8.7 1275 10 CL033318 Arabidops  
C 44 146.4 8.7 1364 10 CG757986 Arabidops  
45 146.2 8.7 939 5 BY720774 Arabidops

#### ALIGNMENTS

RESULT 1  
ATH517160  
LOCUS Arabidopsis thaliana GSS, clone 22B/77, DNA linear GSS 22-NOV-2002  
DEFINITION Arabidopsis thaliana GSS, clone 22B/77, genomic survey sequence.  
ACCESSION AJ517160  
VERSION AJ517160.1 GI:25252960  
KEYWORDS GSS; genome survey sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
REFERENCE 1 (bases 1 to 815)  
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.  
TITLE An Arabidopsis promoter activation-tagged flanking sequence  
JOURNAL Collection (AATSTC)  
REFERENCE 2 (bases 1 to 815)  
AUTHORS Reiss,B.  
TITLE Direct Submission  
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding  
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany  
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Query Match 16.7%; Score 280; DB 10; Length 815;  
Best Local Similarity 100.0%; Pred. No. 3.2e-29;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 319 CTCATCTAGCCCCCATTGGAGCTGAATGTAGACACGTCGAAATAAGATTCCGAATT 378  
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QY 379 AGAATAATTGTTTATGCTTTCCCTATAAATACGACGATCGTAATTGTCGTTTAT 438  
DB 213 AGAATAATTGTTTATGCTTTCCCTATAAATACGACGATCGTAATTGTCGTTTAT 272  
QY 439 CAAATGTACTTTTCATTTTATAAATACGTCGACATCTACATTTTGAATTTGAAAAA 498

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Db 273 CAAATGTACTTTCTTTTATAATACGCTGGGACATCTACATTTTGAATTGAAAAA 332
Qy 499 AATTGTAATTAATCTTTCTTTTCCATATTGACCATCACTCAATTTGCTGATCCATG 558
Db 333 AATTGTAATTAATCTTTCTTTTCCATATTGACCATCACTCAATTTGCTGATCCATG 392
Qy 559 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 598
Db 393 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 432

RESULT 2
ATH517094/c
LOCUS Arabidopsis thaliana GSS, clone 22B/469, genomic survey sequence.
DEFINITION Arabidopsis thaliana GSS, clone 22B/469, genomic survey sequence.
ACCESSION AJ517094
VERSION AJ517094.1 GI:25252831
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 865)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL collection (AATSTC)
REFERENCE 2 (bases 1 to 865)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
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Best Local Similarity 100.0%; Pred. No. 3.2e-29;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 CTCATCTAAGCCCCCATTTGGACGTAATGTAGACACGTCGAAATAAAGATTTCGGAATT 378
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Qy 379 AGAATAATTTGTTTATTGCTTTCCGCTATAAATACGCGATCGTAATTTGCTGTTTAT 438
Db 343 AGAATAATTTGTTTATTGCTTTCCGCTATAAATACGCGATCGTAATTTGCTGTTTAT 284

Qy 439 CAAAATGTAATTTCAATTTTATAATACGCTGGGACATCTACATTTTCAATTTGAAAAA 498
Db 283 CAAAATGTAATTTCAATTTTATAATACGCTGGGACATCTACATTTTCAATTTGAAAAA 224

Qy 499 AATTGTAATTAATCTTTCTTTTCCATATTGACCATCACTCAATTTGCTGATCCATG 558
Db 223 AATTGTAATTAATCTTTCTTTTCCATATTGACCATCACTCAATTTGCTGATCCATG 164

Qy 559 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 598
Db 163 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 124

RESULT 3
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LOCUS Arabidopsis thaliana GSS, clone 22B/658, genomic survey sequence.
DEFINITION Arabidopsis thaliana GSS, clone 22B/658, genomic survey sequence.
ACCESSION AJ516972
VERSION AJ516972.1 GI:25252596
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KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 956)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL collection (AATSTC)
REFERENCE 2 (bases 1 to 956)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
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Best Local Similarity 100.0%; Pred. No. 3.1e-29;
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Qy 319 CTCATCTAAGCCCCCATTTGGACGTAATGTAGACACGTCGAAATAAAGATTTCGGAATT 378
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Qy 379 AGAATAATTTGTTTATTGCTTTCCGCTATAAATACGCGATCGTAATTTGCTGTTTAT 438
Db 231 AGAATAATTTGTTTATTGCTTTCCGCTATAAATACGCGATCGTAATTTGCTGTTTAT 172

Qy 439 CAAAATGTAATTTCAATTTTATAATACGCTGGGACATCTACATTTTCAATTTGAAAAA 498
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Qy 499 AATTGTAATTAATCTTTCTTTTCCATATTGACCATCACTCAATTTGCTGATCCATG 558
Db 111 AATTGTAATTAATCTTTCTTTTCCATATTGACCATCACTCAATTTGCTGATCCATG 52

Qy 559 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 598
Db 51 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 12

RESULT 4
ATH517056
LOCUS Arabidopsis thaliana GSS, clone 22B/820, genomic survey sequence.
DEFINITION Arabidopsis thaliana GSS, clone 22B/820, genomic survey sequence.
ACCESSION AJ517056
VERSION AJ517056.1 GI:25252758
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1146)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL collection (AATSTC)
REFERENCE 2 (bases 1 to 1146)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
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Best Local Similarity 91.8%; Pred. No. 6.9e-29;
Matches 293; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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QY 379 AGAATAATTTGTTTATTTGCTTTCGCCCTATAAATACGACGATCTACATTTTGAATTTGATAT 438
DB 125 AGAATAATTTGTTTATTTGCTTTCGCCCTATAAATACGACGATCTACATTTTGTGCTTTTAT 184

QY 439 CAAAATGTACTTTCATTTTATAAATAGCGCTGCGGACATCTACATTTTGAATTTGAAAAA 498
DB 185 CAAAATGTACTTTCATTTTATAAATAGCGCTGCGGACATCTACATTTTGAATTTGAAAAA 244

QY 499 AATTGGTAATCTCTTTTCTCCATATTGACATCATCTATCTGATCCATG 558
DB 245 AATTGGTAATCTCTTTCTCTCCATATTGACATCATCTATCTGATCCATG 304

QY 559 TAGATTCCCGGACATGAAGCCATTTTACATTTGAATATATATTTACAAGCTATTTGCTTA 618
DB 305 TAGATTCCCGGACATGAAGCCATTTTACATTTGAATATATATTTACAAGCTATTTGCTTA 364

QY 619 TAAATATGCGAAAAATTT 637
DB 365 TATCTTCGCAAGACCTT 383

RESULT 5
ATHS17085/c
LOCUS ATHS17085 863 bp DNA linear GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/472, genomic survey sequence.
ACCESSION AJ517085
VERSION AJ517085.1 GI:25252813
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 863)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 863)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
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Best Local Similarity 97.2%; Pred. No. 3e-26;
Matches 274; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY 319 CTCATCTAAGCCGCCCATTTGGAGCTGAATGTAGACACGTCGAAATAAGATTTCGGAATT 378
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Db 314 TAGATTTCCTGACGAGAACCAACCAACGCTTTGAAATCGAAACAGACAGATATCATCA 373
QY 619 TAAC 622
Db 374 GAAC 377

RESULT 7
ATHS17045
LOCUS Arabidopsis thaliana GSS, clone 22B/83, linear GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/83, genomic survey sequence.
ACCESSION AJ517045
VERSION AJ517045.1 GI:25252736
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1601)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
collection (AATSTC)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1601)
AUTHORS Reiss,B.
DIRECT SUBMISSION Direct Submission
SUBMITTED (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
LOCATION/QUALIFIERS Location/Qualifiers
FEATURES
source
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Best Local Similarity 90.1%; Pred. No. 5.8e-26;
Matches 274; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 319 CTCATCTAAGCCCCCATTTGGAGCTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378
Db 74 CTCATCTAAGCCCCCATTTGGAGCTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 133

QY 379 AGAATAATTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGCTGTTTAT 438
Db 134 AGAATAATTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGCTGTTTAT 193

QY 439 CAAAATGTACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 498
Db 194 CAAAATGTACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 253

QY 499 AATTGGTAATTACTCTTTCTTTCTCCATATTGACCATCATCTATTGCTGATCCATG 558
Db 254 AATTGGTAATTACTCTTTCTTTCTCCATATTGACCATCATCTATTGCTGATCCATG 313

QY 559 TAGATTTCGCGACATGAAGCCATTTACAAATGAATATATATTACAAAGCTATTTGCTTA 618
Db 314 TAGATTTCGCGACATGAAGCCATTTACAAATGAATATATATTACAAAGCTATTTGCTTA 622

QY 619 TAAC 622
Db 374 GAAC 377

RESULT 8
ATHS17113/c
LOCUS Arabidopsis thaliana GSS, clone 22B/746, linear GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/746, genomic survey sequence.
ACCESSION AJ517113
VERSION AJ517113.1 GI:25252867
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KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 808)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
collection (AATSTC)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 808)
AUTHORS Reiss,B.
DIRECT SUBMISSION Direct Submission
SUBMITTED (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
LOCATION/QUALIFIERS Location/Qualifiers
FEATURES
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1..808
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/mol_type="genomic DNA"
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/clone="22B/746"
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ORIGIN
Query Match 13.2%; Score 221.2; DB 10; Length 808;
Best Local Similarity 80.7%; Pred. No. 4.2e-21;
Matches 226; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 319 CTCATCTAAGCCCCCATTTGGAGCTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378
Db 291 CTCATCTAAGCCCCCATTTGGAGCTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 232

QY 379 AGAATAATTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGCTGTTTAT 438
Db 231 AGAATAATTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGCTGTTTAT 172

QY 439 CAAAATGTACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 498
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QY 499 AATTGGTAATTACTCTTTCTTTCTCCATATTGACCATCATCTATTGCTGATCCATG 558
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QY 559 TAGATTTCGCGACATGAAGCCATTTACAAATGAATATATATTACAAATGAATATAT 598
Db 51 TAGATTTCGCGACATGAAGCCATTTACAAATGAATATATATATATATATATATAT 12

RESULT 9
ATHS16966/c
LOCUS Arabidopsis thaliana GSS, clone 22B/774, linear GSS 12-MAR-2003
DEFINITION Arabidopsis thaliana GSS, clone 22B/774, genomic survey sequence.
ACCESSION AJ516966
VERSION AJ516966.1 GI:25252584
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 970)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
collection (AATSTC)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 970)
AUTHORS Reiss,B.
DIRECT SUBMISSION Direct Submission
SUBMITTED (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
LOCATION/QUALIFIERS Location/Qualifiers
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Best Local Similarity 96.4%; Pred. No. 9.8e-21;
Matches 244; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
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Db 260 CTCATCTAAGCCCCCATTTGACGTGAATGTAGACACGTGCAATGAATTCGGAATT 201
QY 379 AGAATAATTTGTTTATTTGCTTTCGCCCTATAAATACGACGATCGTAATTTGCTGTTTAT 438
Db 200 AGAATAATTTGTTTATTTGCTTTCGCCCTATAAATACGACGATCGTAATTTGCTGTTTAT 141
QY 439 CAAATGTACTTTCATTTTAAATACGCTCGGACATCTACATTTTGAATTTGAAAAA 498
Db 140 CAAATG-ACATTCATTTTAAATACGCTCGGACATCAACATTTTGAATTTGAAAAA 82
QY 499 AATGGTAATTAAT-CTTCTTTTCTCCATTTGACCATCATCTCATTTGCTGATCCAT 557
Db 81 AATGGTAATTAATCTCCCTTTTCTCCATTTGACCATCATCTCATTTGCTGATCCAT 22
QY 558 GTAGATTTCCCG 570
Db 21 GTAGATTTCCGG 9

RESULT 10
ATH516980/c
LOCUS ATH516980 975 bp DNA linear GSS 12-MAR-2003
DEFINITION Arabidopsis thaliana GSS, clone 22B/557, genomic survey sequence.
ACCESSION AJ516980
VERSION AJ516980.1 GI:25252612
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 975)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
collection (AATSTC)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES
source
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/clone="22B/557"
/note="ecotype: Columbia"

ORIGIN
Query Match 12.0%; Score 201; DB 10; Length 975;
Best Local Similarity 87.4%; Pred. No. 2.5e-18;
Matches 236; Conservative 0; Mismatches 31; Indels 3; Gaps 2;
QY 320 TCATCTAAGCCCCCATTTGACGTGAATGTAGACACGTGCAATGAATTCGGAATTA 379
Db 277 TCATNTAAGCCCCCATTTGACGTGAATGTAGACACGTGCAATGAATTCGGAATTA 218
QY 380 GAATAATTTGTTTATTTGCTTTCGCCCTATAAATACGACGATCGTAATTTGCTGTTTAT 437

Db 217 GGATAATTTGTTTATTTGCTTTCGCCCTATAAATACGACGATCGTAATTTGCTGTTTATC 158
QY 438 TCAAAATGTACTTTTCATTTTATAAATACGCTCGGACATCTACATTTTTCGAATTTGAAAAA 497
Db 157 TCAATGGACCTTCTCTTTTATAAATACGCTCGGACATCTACATTTTGTATTTGAAAAA 98
QY 498 AAATGGTAATTAATCTCTTTTCTCCATTTGACCATCATCTCATTTGCTGATCCAT 557
Db 97 AAATGG-GANCCCTCTTTTCTCCATTTGACCATCATCTCATTTGCTGATCCAT 39
QY 558 GTAGATTTCCCGACATGAAGCCATTTACA 587
Db 38 GTAGATTTCCCGACATGAAGCCATTTNAA 9

CG753083 1896 bp DNA linear GSS 24-OCT-2003
P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
CG753083
CG753083.1 GI:37977199
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 1896)
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus
pacificus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
FEATURES
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the genomic DNA with EcoRI and cloning into the BAC
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Query Match 10.1%; Score 169.8; DB 10; Length 1896;
Best Local Similarity 50.2%; Pred. No. 4.4e-14;
Matches 457; Conservative 0; Mismatches 449; Indels 4; Gaps 3;
QY 693 AAATGAAAAATTTCTTATTTAGTTTAAATTTTAAAGTAAAAATATAAAAAATTTTCAT 752
Db 250 ATATTTTATTTTAAATTAATAAATAAATAATATATATATATATATATATATATATATAT 309
QY 753 TTAATCCTTTAAATAATATAAGATAT-AGCATTTAAATATGATGAAATATACATTTTAT 811
Db 310 TTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 369
QY 812 TATCATAAAAATTTATTTATTTTAAATTTTTCGACCCCTAACAAAAATTTCTGATTTTTCGCCCTAA 871
Db 370 TATTTAATAATTAATAATTTTATTTATTTAATAATTAATAATTTTATTTAATAATTAATAATA 429
QY 872 CTGTATATTTTGTATAAAAACATTTTCTTTTTCATTTTAATGATTTCTTTTAATTCAGTCC 931
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430 TATTATTATATTATTAATAAATAATATAAATAATATTTAATAATAATAATAATAATATTAATNT 489  
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QY 992 AAGAAACATAAATAATCAATAAATAATTTTAAAGCAATAGTAAATAAAGCAAACT 1051  
Db 550 TATATATTTATTTATTAATTAATTAATTAATTTATTAATAAANANNTTTATTTATATATA 609  
QY 1052 TTCTACGATAGTCTATAATTTCAAAAAAGAAATAAATCTTTAACCAATGAATTTAAA 1111  
Db 610 TTTTAAATAATNATAATTTTATAAATAATTTATATAATTTTNNATAATTTATATATATTTATTA 669  
QY 1112 ATACATCAGATATCTATTTATTTAATTTAATAAATAATTAATAATTAACATATATATATA 1171  
Db 670 ATAATAAATAAATAAATAATATATATATTTTAAATTTTATTTTAAATTTTATTTATTA 729  
QY 1172 TTAATAATTTTATGAGCTTAGTGCACAAATCAATAAATAAATTTCTTCAAAATAAAT 1231  
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Db 790 ATTATATTTTAAATTTTATTAATTTTNNATNATAAATTTATATAAATAATATATATTTA 849  
QY 1292 ATACATATATAAATTTGAATCCAAATTTTAAATTTTAAACAT-TTATAATTTACTATT 1350  
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QY 1351 CAACCAAAATTTTATTTATTTATATATCAAAATTTTATAAATAATTTATATCAGATAATG 1410  
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QY 1469 ATATATATACACAAATAATTTCTTAAATGATCTGATATATCTTAAACCCCTTTTATAA 1528  
Db 1030 AATATATAAANAATAATATAATTTATATATAAATAAATAAATAATTTATATATTTTAAATA 1089  
QY 1529 AACAATCTTAAACCCCTATATATTTTAAATTAATATATCATATATAAATAAATCTATGCA 1588  
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QY 1589 GCATATGTTT 1598  
Db 1150 TTTTATTTAT 1159

RESULT 12  
LOCUS CK997149  
DEFINITION 1313 bp mRNA linear EST 26-MAR-2004  
ip15c02.b1 Brain - Cerebellum Library (DOEST8) Canis familiaris  
CDNA clone ip15c02, mRNA sequence.  
ACCESSION CK997149  
VERSION CK997149.1 GI:45760829  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
REFERENCE 1 (bases 1 to 1313)  
AUTHORS Ballia,V., Nascimben,L.U. and McCombie,W.R.  
TITLE ESTs from Canis familiaris cerebellum (dog)  
JOURNAL Unpublished (2004)  
COMMENT Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884

Fax: 516 367 8874  
Email: mcombie@cshl.org  
Plate: ip15 row: c column: 02  
High quality sequence stop: 1313.  
Location/Qualifiers  
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/note="Organ: Brain; Vector: pBluescript II SK; Site 1:  
XR kit; Site 2: XhoI; Library constructed using plusescript  
XR kit from Stratagene. Cloned cDNA was size selected  
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and  
Medical Genetics, School of Veterinary Medicine,  
University of Pennsylvania, 3800 Spruce Street,  
Philadelphia, PA 19104-6051"

## ORIGIN

Query Match 10.1%; Score 169; DB 7; Length 1313;  
Best Local Similarity 49.1%; Pred. No. 6e-14;  
Matches 571; Conservative 0; Mismatches 566; Indels 25; Gaps 5;  
QY 426 TTTGCTGTTTATCAAAATGTAATTTTCAATTTTATAAATGCTGCGGACATCTCACATTTT 485  
Db 162 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 221  
QY 486 TGAATGAAAAAATGTAATTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 545  
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QY 546 TTGCTGATCCATGATGATTTCCGGACATGAAGCCATTTTACAATGCAATATATATATACAA 605  
Db 282 TATATAATATATATTAATTTTATTTTAAATTAATAAATAAATAAATAAATAAATAAATA 341  
QY 606 AGCTATTTGCTTTATACATATCGAAAAATTTTGTACTATAATCAGGGGTAAATTTTAGGA 665  
Db 342 TTTTATATTTATTAATAATTTATTTTATATTTTATTTTATTTTATTTTATTTTATTTA 401  
QY 666 GGGGGCTGTAGGTCTGCTTCTTTAAATGAAAAATTTTCTATTTAGTTATTTTAAAT 725  
Db 402 AATTAATAAATAATATATATTTTCTTTTAAATAAATAAATAAATAAATAAATAAATA 453  
QY 726 TTTAAAGTAAATATATAAATAATTTCTATTTAAATCTTTTAAATAATATAAAGATATAGACTA 785  
Db 454 ATTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 513  
QY 786 TTAATAATGATGAAATTTACAAATTTTATTTATCATATAAATAATTTAATTTTAAATTTT 845  
Db 514 ATATATATATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 573  
QY 846 ACAAAATTTTCTGATTTTTCGCCCTTAACGTGATATTTGTATATAAACAATTTTCTTTTTC 905  
Db 574 AAAAAATTTTNTTATTTTAAATTTAAATAATATATATAAATAAATAAATAAATAAATAA 633  
QY 906 ATTTAATGATTTCTTTTAAATTTTCAAGTCAAGAAAGAAATTTTAAATTTGATATGCGAAAGT 965  
Db 634 AAAAAATAAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 693  
QY 966 TAGTCTTCTGCTAGTATTAATAAGGAAAGAAACAT-----AAATCAATAAATAAAT 1018  
Db 694 AATTTTATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 753  
QY 1019 TTTTAAAGCAATAGTAAATAAATAAAGGAAACCTTTCTAGATAGTCTATAATTTCAAAAAA 1078  
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QY 1461 CTAAAAATAATATATCATACCAAAAAAATCTTAAATGATCTGATATCTTAACCCC 1520  
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RESULT 14  
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 LOCUS  
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-304N17.TJ, genomic survey sequence.  
 ACCESSION AG430010  
 VERSION AG430010.1 GI:48073073  
 KEYWORDS GSS.  
 SOURCE Mus musculus molossinus (Japanese wild mouse)  
 ORGANISM Mus musculus molossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
 AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T., Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriaki,K. and Shiroishi,T.  
 TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis  
 JOURNAL Genome Res. 14 (12), 2439-2447 (2004)  
 PUBMED 15574823

REFERENCE 2 (bases 1 to 1227)  
 AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)  
 COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp

PRIMERS  
 Sequencing : TJ  
 LIBRARY  
 Vector : pBACe3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI  
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ORIGIN

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 QY 587 AATCGAATATATATATCAAGCTATTTGCTTATAACATATGCGAAAAATTTTGTACTATA 646  
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 QY 647 ATCAGGGTAAATTTAGGAGGGGCTTGTAGTCTCGCTTCTTTAAATGAAAAATTTT 706  
 Db |||||  
 1142 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 1084  
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 1083 AAATAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1024  
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 903 AAAAAAATAATATATATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 844  
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 791 AAAAAAATAATTTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 732  
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 731 TAAAAATATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 672  
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 611 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 552  
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 551 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 492  
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 431 NTATATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 372  
 QY 1422 ACCTATATATAGATGACATAATCTACTTTAAATTTAAAGTCTAAATAAATAAATAA 1481  
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 371 ATATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 312  
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 311 ATTTTATTTTAT 252  
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 251 CACACTAT 208



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RESULT 15
ATH517144
LOCUS      ATH517144      820 bp      DNA      linear      GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/398, genomic survey sequence.
ACCESSION  AJ517144
VERSION    AJ517144.1 GI:25252928
KEYWORDS   GSS; genome survey sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 820)
AUTHORS   Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE     An Arabidopsis promoter activation-tagged flanking sequence
          collection (AATSTC)
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 820)
AUTHORS   Reiss,B.
TITLE     Direct Submission
JOURNAL   Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
          Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES   Location/Qualifiers
            source
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                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /db_xref="taxon:3702"
                /clone="22B/398"
                /ecotype="Columbia"

ORIGIN
Query Match      9.7%; Score 162.2; DB 10; Length 820;
Best Local Similarity 92.6%; Pred. No. 5.7e-13;
Matches 200; Conservative 0; Mismatches 13; Indels 3; Gaps 3;

QY 319 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCGGAATT 378
Db 319 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCGGAATT 378
QY 598 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCGGAATT 657
Db 598 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCGGAATT 657
QY 379 AGAATAAATTTGTTTATTCG- TTTCGCCTATAAATACGACGGATCGTAATTT-GTCGTTTT 436
Db 379 AGAATAAATTTGTTTATTCG- TTTCGCCTATAAATACGACGGATCGTAATTT-GTCGTTTT 436
QY 437 ATCAAAATGTACTTTTCATTTTATAATAA-CGCTCGGACATCTACATTTTGAATTGAAA 495
Db 437 ATCAAAATGTACTTTTCATTTTATAATAA-CGCTCGGACATCTACATTTTGAATTGAAA 495
QY 718 ATCAAAATGTACTTTTCATTTTATAATAAAGCGCTCGGACATTTACATTTTGAATTGGAA 777
Db 718 ATCAAAATGTACTTTTCATTTTATAATAAAGCGCTCGGACATTTACATTTTGAATTGGAA 777
QY 496 AAAAAATTGGTAATCTCTTTCTTTTCTCCATATT 531
Db 496 AAAAAATTGGTAATCTCTTTCTTTTCTCCATATT 531
QY 778 AAAAAATTGGNAATTACTTCTTCTTTTCTTCTCTCTNAT 813
Db 778 AAAAAATTGGNAATTACTTCTTCTTTTCTTCTCTCTNAT 813
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Search completed: March 31, 2006, 12:24:23  
Job time : 7674.01 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 30, 2006, 14:04:38 ; Search time 552.987 Seconds  
(without alignments)  
5384.242 Million cell updates/sec

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Perfect score: 1675  
Sequence: 1 tgaccgaagtaatatgagg.....tagtgcgaacctggagaag 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	310	18.5	8012	3	US-09-182-117-1
2	310	18.5	8012	3	US-09-434-039A-1
3	310	18.5	8418	3	US-09-182-117-5
4	310	18.5	8418	3	US-09-434-039A-5
5	310	18.5	8798	3	US-09-182-117-4
6	310	18.5	8798	3	US-09-434-039A-4
7	310	18.5	10846	3	US-09-098-219B-5
8	310	18.5	10846	3	US-10-164-204-5
9	310	18.5	10846	3	US-09-923-109-5
10	310	18.5	10900	3	US-09-098-219B-6
11	310	18.5	10900	3	US-10-164-204-6
12	310	18.5	10900	3	US-09-923-109-6
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14	282	16.8	632	3	US-10-015-637-7
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18	280.2	16.7	10339	3	US-09-186-002-13
19	280.2	16.7	14194	3	US-09-577-424-3
20	280.2	16.7	15397	2	US-08-673-768-1
C 21	280.2	16.7	24595	9	5428147-1
C 22	280.2	16.1	10323	3	US-09-280-428A-11
23	153.2	9.1	187169	3	US-09-949-016-12776
24	153.2	9.1	191569	3	US-09-949-016-15940

25	149.4	8.9	18773	3	US-09-949-016-14164	Sequence 14164, A
26	146.2	8.7	11978	3	US-09-792-568-8	Sequence 8, Appli
27	146.2	8.7	12438	3	US-09-792-568-9	Sequence 9, Appli
C 28	136.2	8.1	18773	3	US-09-949-016-14164	Sequence 14164, A
C 29	133.4	8.0	30820	3	US-09-949-016-17145	Sequence 17145, A
C 30	123.4	7.4	50000	3	US-09-662-254B-23	Sequence 23, Appli
C 31	122.4	7.3	30820	3	US-09-949-016-17145	Sequence 17145, A
C 32	121.6	7.3	32392	3	US-09-662-254B-27	Sequence 27, Appli
C 33	121.2	7.2	187169	3	US-09-949-016-12776	Sequence 12776, A
C 34	121.2	7.2	191569	3	US-09-949-016-15940	Sequence 15940, A
C 35	120.6	7.2	95255	3	US-09-949-016-17067	Sequence 17067, A
C 36	119.4	7.1	12313	3	US-09-949-016-13248	Sequence 13248, A
C 37	118.8	7.1	119153	3	US-09-949-016-12378	Sequence 12378, A
C 38	118.4	7.1	95255	3	US-09-949-016-17067	Sequence 17067, A
C 39	117.6	7.0	50000	3	US-09-662-254B-23	Sequence 23, Appli
C 40	116.4	6.9	134987	3	US-09-949-016-15348	Sequence 15348, A
C 41	116.4	6.9	134987	3	US-09-949-016-15349	Sequence 15349, A
C 42	116.4	6.9	134987	3	US-09-949-016-15350	Sequence 15350, A
C 43	116.4	6.9	134987	3	US-09-949-016-15307	Sequence 15307, A
C 44	116.4	6.9	134987	3	US-09-949-016-15508	Sequence 15508, A
C 45	116.4	6.9	134987	3	US-09-949-016-15509	Sequence 15509, A

ALIGNMENTS

RESULT 1

US-09-182-117-1  
; Sequence 1, Application US/09182117  
; Patent No. 6204436  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Transgenic Plant  
; NUMBER OF SEQUENCES: 27  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/182,117  
; FILING DATE:  
; CLASSIFICATION:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8012 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-182-117-1

Query Match 18.5%; Score 310; DB 3; Length 8012;  
Best Local Similarity 100.0%; Pred. No. 2.8e-42;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TGACCAAGTTATATGAGGAGTAAACACATCTTGTAGTGTACCATTTGCTTATTCCTACTA	60
DB	2708	TGACCAAGTTATATGAGGAGTAAACACATCTTGTAGTGTACCATTTGCTTATTCCTACTA	2767
QY	61	GGCAACAATATATTTTTCAGACCTAGAAAGCTGCAAAAGTCTTACTGTAATACAAAGTATGTC	120
DB	2768	GGCAACAATATATTTTTCAGACCTAGAAAGCTGCAAAAGTCTTACTGTAATACAAAGTATGTC	2827
QY	121	CTCTGTGTTTTAGACATTTATGACATTTCTTCTTATGTATATTTTCCAGAAATCCTTGTTCAG	180
DB	2828	CTCTGTGTTTTAGACATTTATGACATTTCTTCTTATGTATATTTTCCAGAAATCCTTGTTCAG	2887
QY	181	ATTCTAATCATTCCTTTTATTAATTTATAGTTATATCTATGATGATTTGTAGTTAGTATGAAAA	240
DB	2888	ATTCTAATCATTCCTTTTATTAATTTATAGTTATATCTATGATGATTTGTAGTTAGTATGAAAA	2947



Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACACTGTGTAGTTGACCAATATGCTTATTCACCTA 60  
Db 2687 TGACCGAAGTTAATATGAGGAGTAAACACACTGTGTAGTTGACCAATATGCTTATTCACCTA 2746

Qy 61 GGCACAAATATATTTTCAGACCTTAGAAAAGCTGCAATGTTACTGAATCAAGTATGTC 120  
Db 2747 GGCACAAATATATTTTCAGACCTTAGAAAAGCTGCAATGTTACTGAATCAAGTATGTC 2806

Qy 121 CTCCTGTGTTTTAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180  
Db 2807 CTCCTGTGTTTTAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 2866

Qy 181 ATTCTAATCAATGCTTTTATATATTAATAGTATATACCTGCAATGTTGAGTATGAGTATGAAAA 240  
Db 2867 ATTCTAATCAATGCTTTTATATATTAATAGTATATACCTGCAATGTTGAGTATGAGTATGAAAA 2926

Qy 241 TATTTTAAATGCAATTTTATGACCTTGCCAAATGATTGACAACTGCAATGCAATCGACCTGC 300  
Db 2927 TATTTTAAATGCAATTTTATGACCTTGCCAAATGATTGACAACTGCAATGCAATCGACCTGC 2986

Qy 301 AGCCACTCGA 310  
Db 2987 AGCCACTCGA 2996

## RESULT 5

US-09-182-117-4

; Sequence 4, Application US/09182117

; Patent No. 6204436

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Transgenic Plant

; NUMBER OF SEQUENCES: 27

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION NUMBER: US/09/182,117

; FILING DATE:

; CLASSIFICATION:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8798 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-09-182-117-4

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e-42; Length 8798;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACACTGTGTAGTTGACCAATATGCTTATTCACCTA 60  
Db 2797 TGACCGAAGTTAATATGAGGAGTAAACACACTGTGTAGTTGACCAATATGCTTATTCACCTA 2856

Qy 61 GGCACAAATATATTTTCAGACCTTAGAAAAGCTGCAATGTTACTGAATCAAGTATGTC 120  
Db 2857 GGCACAAATATATTTTCAGACCTTAGAAAAGCTGCAATGTTACTGAATCAAGTATGTC 2916

Qy 121 CTCCTGTGTTTTAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180  
Db 2917 CTCCTGTGTTTTAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 2976

Qy 181 ATTCTAATCAATGCTTTTATATATTAATAGTATATACCTGCAATGTTGAGTATGAGTATGAAAA 240  
Db 2987 ATTCTAATCAATGCTTTTATATATTAATAGTATATACCTGCAATGTTGAGTATGAGTATGAAAA 3036

Db 2977 ATTCTAATCAATGCTTTTATATTAATTAATAGTATATACCTGCAATGTTGAGTATGAGTATGAAAA 3036

Qy 241 TATTTTAAATGCAATTTTATGACCTTGCCAAATGATTGACAACTGCAATGCAATCGACCTGC 300  
Db 3037 TATTTTAAATGCAATTTTATGACCTTGCCAAATGATTGACAACTGCAATGCAATCGACCTGC 3096

Qy 301 AGCCACTCGA 310  
Db 3097 AGCCACTCGA 3106

## RESULT 6

US-09-434-039A-4

; Sequence 4, Application US/09434039A

; Patent No. 6531649

; GENERAL INFORMATION:

; APPLICANT: MANNERLOEF, Marie

; APPLICANT: TENNING, Paul Peter

; APPLICANT: STEEN, Per

; TITLE OF INVENTION: Transgenic Plants

; FILE REFERENCE: 09/434,039

; CURRENT APPLICATION NUMBER: US/09/434,039A

; CURRENT FILING DATE: 1999-11-04

; PRIOR APPLICATION NUMBER: 60/112,003

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 09/182,117

; PRIOR FILING DATE: 1998-10-29

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 4

; LENGTH: 8798

; TYPE: DNA

; ORGANISM: Sugar beet

; US-09-434-039A-4

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e-42; Length 8798;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACACTGTGTAGTTGACCAATATGCTTATTCACCTA 60  
Db 2797 TGACCGAAGTTAATATGAGGAGTAAACACACTGTGTAGTTGACCAATATGCTTATTCACCTA 2856

Qy 61 GGCACAAATATATTTTCAGACCTTAGAAAAGCTGCAATGTTACTGAATCAAGTATGTC 120  
Db 2857 GGCACAAATATATTTTCAGACCTTAGAAAAGCTGCAATGTTACTGAATCAAGTATGTC 2916

Qy 121 CTCCTGTGTTTTAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180  
Db 2917 CTCCTGTGTTTTAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 2976

Qy 181 ATTCTAATCAATGCTTTTATATTAATTAATAGTATATACCTGCAATGTTGAGTATGAGTATGAAAA 240  
Db 2977 ATTCTAATCAATGCTTTTATATTAATTAATAGTATATACCTGCAATGTTGAGTATGAGTATGAAAA 3036

Qy 241 TATTTTAAATGCAATTTTATGACCTTGCCAAATGATTGACAACTGCAATGCAATCGACCTGC 300  
Db 3037 TATTTTAAATGCAATTTTATGACCTTGCCAAATGATTGACAACTGCAATGCAATCGACCTGC 3096

Qy 301 AGCCACTCGA 310  
Db 3097 AGCCACTCGA 3106

## RESULT 7

US-09-098-219B-5

; Sequence 5, Application US/09098219B

; Patent No. 6441277

; GENERAL INFORMATION:

; APPLICANT: Barry, Gerard

; APPLICANT: Cheikh, No. 6441277dine

; APPLICANT: Kishore; Ganesh

; TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate

```

/ TITLE OF INVENTION: Adolase in Transgenic Plants
/
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: Arnold White & Durkee
/ STREET: P. O. Box 4433
/ CITY: Houston
/ STATE: TX
/
/ COUNTRY: US
/ ZIP: 77210-4433
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA: US/09/098,2198
/
/ FILING DATE:
/
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/049,995
/
/ FILING DATE: 17-JUN-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kammerer, Patricia A.
/
/ REGISTRATION NUMBER: 29,775
/
/ REFERENCE/DOCKET NUMBER: MOBT.086
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713-787-1400
/ TELEFAX: 713-787-1440
/
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10846 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/
/ US-09-098-2198-5

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Query Match	18.5%	Score 310	DB 3	Length 10846
Best Local Similarity	100.0%	Pred. No. 2.8e-42		
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DB	2059	TGACCGAAGTTAATATGAGGAGTAAACACCTGTAGTTGTACCATATGCTTATTCACCTA	2118	
QY	61	GGCAACAAATATATTTTCAGACCTAGAAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC	120	
DB	2119	GGCAACAAATATATTTTCAGACCTAGAAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC	2178	
QY	121	CTCTTGTTTTAGACATTTATGAACCTTCCTTTATGTAAATTTTCCAGAATCCTTGTGCAG	180	
DB	2179	CTCTTGTTTTAGACATTTATGAACCTTCCTTTATGTAAATTTTCCAGAATCCTTGTGCAG	2238	
QY	181	ATTCTAATCATTCCTTTTATAAATTTATAGTTATCTCATGGATTTGTAGTTCAGATATGAAA	240	
DB	2239	ATTCTAATCATTCCTTTTATAAATTTATAGTTATCTCATGGATTTGTAGTTCAGATATGAAA	2298	
QY	241	TATTTTTTAATGCATTTTATGACTTGCCAATTGATTGACAAACATGTCATCAATCGACCTGC	300	
DB	2299	TATTTTTTAATGCATTTTATGACTTGCCAATTGATTGACAAACATGTCATCAATCGACCTGC	2358	
QY	301	AGCCACTCGA	310	
DB	2359	AGCCACTCGA	2368	

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RESULT 8
US-10-164-204-5
; Sequence 5, Application US/10164204
; Patent No. 6663906
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard
; APPLICANT: Cheikh, No. 6663906din
; APPLICANT: Kishore, Ganesh

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; TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Trans
; FILE REFERENCE: 11899.0086.DVUS02 (NOB:086-2)
; CURRENT APPLICATION NUMBER: US/10/164,204
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/098,219
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10846
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P-FMV/CTP1/fda/NOS3',
US-10-164-204-5

Query Match      18.5%; Score 310; DB 3; Length 10846;
Best Local Similarity 100.0%; Pred.No.2.8e-42;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      TGACCGAAGTTAATATGAGGAGTAAAAACACTTGTAGTTGTACCATTTATGCTTATTACACTA 60
Db      2059   TGACCGAGTTAATATGAGGAGTAAACACTTGTAGTTGTACCATTTATGCTTATTACACTA 2118

Qy      61      GGCAACAATATATTTTCAGACCTAGAAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 120
Db      2119   GGCAACAATATATTTTCAGACCTAGAAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 2178

Qy      121     CTCTTGTTGTTTATAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGATCCTTGTGCAG 180
Db      2179   CTCTTGTTGTTTATAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGATCCTTGTGCAG 2238

Qy      181     ATTCTAATCATTCCTTTTATAATTTATATAGTTTATACTCATGGATTTGTAGTTGAGTATGAAAA 240
Db      2239   ATTCTAATCATTCCTTTTATAATTTATATAGTTTATACTCATGGATTTGTAGTTGAGTATGAAAA 2298

Qy      241     TATTTTTTAATGCATTTTATGACTTCGCAATTGCAATTCGATTCAGAACATGCATCAATCGACCTGC 300
Db      2299   TATTTTTTAATGCATTTTATGACTTCGCAATTGCAATTCGATTCAGAACATGCATCAATCGACCTGC 2358

Qy      301     AGGCACCTCGA 310
Db      2359   AGGCACCTCGA 2368

RESULT 9
US-09-923-109-5
; Sequence 5, Application US/09923109
; Patent No. 6716474
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard
;             Cheikh, No. 6716474dine
;             Kishore, Ganesh
; TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate
;                 Aldolase in Transgenic Plants
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,109
; FILING DATE: 06-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 09/098,219  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/049,995  
FILING DATE: 17-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Kammerer, Patricia A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: MOBT:086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-787-1440  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10846 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-923-109-5

Query Match 18.5%; Score 310; DB 3; Length 10846;  
Best Local Similarity 100.0%; Pred. No. 2.8e-42;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATATGCTTATTCACCTA 60  
Db 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATATGCTTATTCACCTA 2118  
Qy 61 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 120  
Db 2119 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 2178  
Qy 121 CTCCTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 180  
Db 2179 CTCCTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 2238  
Qy 181 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTGATGATGAAAA 240  
Db 2239 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTGATGATGAAAA 2298  
Qy 241 TATTTTAAATGCAATTTATGCACTTGCCTGCAATGTTGACATGCAATGCAATGCAATGCAATGCA 300  
Db 2299 TATTTTAAATGCAATTTATGCACTTGCCTGCAATGTTGACATGCAATGCAATGCAATGCAATGCA 2358  
Qy 301 AGCCACTCGA 310  
Db 2359 AGCCACTCGA 2368

## RESULT 10

US-09-098-219B-6  
Sequence 6, Application US/09098219B  
Patent No. 6441277  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard  
APPLICANT: Cheikh, No. 6441277dine  
APPLICANT: Kishore, Ganesh  
TITLE OF INVENTION: Expression of Fructose 1,6 Biphosphatase  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/098,219B  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/049,995  
FILING DATE: 17-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Kammerer, Patricia A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: MOBT:086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-787-1440  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10900 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-098-219B-6

Query Match 18.5%; Score 310; DB 3; Length 10900;  
Best Local Similarity 100.0%; Pred. No. 2.8e-42;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATATGCTTATTCACCTA 60  
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Qy 61 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 120  
Db 2119 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 2178  
Qy 121 CTCCTGTGTTTTAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 180  
Db 2179 CTCCTGTGTTTTAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 2238  
Qy 181 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTGATGATGAAAA 240  
Db 2239 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTGATGATGAAAA 2298  
Qy 241 TATTTTAAATGCAATTTATGCACTTGCCTGCAATGTTGACATGCAATGCAATGCAATGCAATGCA 300  
Db 2299 TATTTTAAATGCAATTTATGCACTTGCCTGCAATGTTGACATGCAATGCAATGCAATGCAATGCA 2358  
Qy 301 AGCCACTCGA 310  
Db 2359 AGCCACTCGA 2368

## RESULT 11

US-10-164-204-6  
Sequence 6, Application US/10164204  
Patent No. 6663906  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard  
APPLICANT: Cheikh, No. 6663906dine  
APPLICANT: Kishore, Ganesh  
TITLE OF INVENTION: Expression of Fructose 1,6 Biphosphatase  
FILE REFERENCE: 11899.0086.DVUS02 (MOBT:086-2)  
CURRENT APPLICATION NUMBER: US/10/164,204  
CURRENT FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: 09/098,219  
PRIOR FILING DATE: 1998-06-16  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 10900  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: P-FMV/CTP2/Eda/NO3'  
US-10-164-204-6





Db 3882 ATTCTAATCATGCTTTTATTAATTATAGTATATCTCATGAGTTTGTAGTATGAAAA 3941  
Qy 241 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCATC 289  
Db 3942 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCATC 3990  
RESULT 14  
US-10-015-637-7  
; Sequence 7, Application US/10015637  
; Patent No. 6927321  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Qi  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Liang, Jihong  
; APPLICANT: Oulmassov, Tim  
; TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof  
; FILE REFERENCE: 13587.106  
; CURRENT APPLICATION NUMBER: US/10/015.637  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: US 60/255879  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 7  
; LENGTH: 632  
; TYPE: DNA  
; ORGANISM: Pisum sp.  
US-10-015-637-7

Query Match 16.8%; Score 282; DB 3; Length 632;  
Best Local Similarity 100.0%; Pred. No. 9.9e-38;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 351 TGACCGAAGTAAATATGAGAGTAAACACTTGTAGTTGTACCATTTATGCTTATTCAC 410  
Qy 61 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAATCTTACTGAATACAAAGTATGC 120  
Db 411 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAATCTTACTGAATACAAAGTATGC 470  
Qy 121 CTCTTGTTGTTTATGACATTTATGAACTTCTCTTATGTAATTTTCCAGAATCCTTGTGCG 180  
Db 471 CTCTTGTTGTTTATGACATTTATGAACTTCTCTTATGTAATTTTCCAGAATCCTTGTGCG 530  
Qy 181 ATTCTAATCATGCTTTTATTAATTATAGTTATATCTCATGAGTTTGTAGTTGAGTATGAAA 240  
Db 531 ATTCTAATCATGCTTTTATTAATTATAGTTATATCTCATGAGTTTGTAGTTGAGTATGAAA 590  
Qy 241 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCATC 282  
Db 591 TATTTTTTAATGCAATTTTATGACTTGCCAAATGATTGACAAATGCATC 632

RESULT 15  
US-08-549-680A-5  
; Sequence 5, Application US/08549680A  
; Patent No. 5962768  
; GENERAL INFORMATION:  
; APPLICANT: CORNELISSEN, MARCUS  
; APPLICANT: REYNAERTS, ARLETTE  
; APPLICANT: GOSSELE, VERONIQUE  
; APPLICANT: VAN AARSEN, ROEL  
; TITLE OF INVENTION: MARKER GENE  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA

ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/549,680A  
FILING DATE: 16 JANUARY 1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 2121-0111P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7811 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (synthetic)  
FEATURE:  
NAME/KEY: misc recomb  
LOCATION: 1..7811  
OTHER INFORMATION: /label= vector ptrVA3  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 194..218  
OTHER INFORMATION: /note= "T-DNA right border"  
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NAME/KEY: misc feature  
LOCATION: 484..684  
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OTHER INFORMATION: polyadenylation region of T-DNA gene 7"  
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LOCATION: complement (729..1340)  
OTHER INFORMATION: /note= "the aac(6') coding  
OTHER INFORMATION: sequence"  
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NAME/KEY: promoter  
LOCATION: 1341..1756  
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FEATURE:  
NAME/KEY: misc feature  
LOCATION: 3001..3023  
OTHER INFORMATION: /note= "T-DNA left border  
OTHER INFORMATION: sequences"  
US-08-549-680A-5

Query Match 16.7%; Score 280.2; DB 2; Length 7811;  
Best Local Similarity 98.9%; Pred. No. 2.1e-37;  
Matches 282; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 319 CTCATCTAAGCCCCCAATTTTGACGCTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378  
Db 2739 CTCATCTAAGCCCCCAATTTTGACGCTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 2798  
Qy 379 AGAATAATTTGTTTATTTGCTTTTCGCCCTATAAATACGACGATCGTAATTTGTGTTTTAT 438  
Db 2799 AGAATAATTTGTTTATTTGCTTTTCGCCCTATAAATACGACGATCGTAATTTGTGTTTTAT 2858  
Qy 439 CAAATGTACTTTTCATTTTATATAACGCTGCGGACATCTACATTTTGTGAATGAAAAA 498  
Db 2859 CAAATGTACTTTTCATTTTATATAACGCTGCGGACATCTACATTTTGTGAATGAAAAA 2918  
Qy 499 AATTGGTAATTACTCTTTTCTTCTCCATATTGACCATCATCTACTCTGTCATCCATG 558  
Db 2919 AATTGGTAATTACTCTTTTCTTCTTCTTCTCCATATTGACCATCATCTACTCTGTCATCCATG 2978



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OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:58:31 ; Search time 1286.41 Seconds  
(without alignments)  
10767.297 Million cell updates/sec

Title: US-10-541-346-4

Perfect score: 1675

Sequence: 1 tgaccgaagtaatatgagg.....tagtgaacctggagaag 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:  
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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	530.6	31.7	3706	7 US-10-376-763A-6	Sequence 6, Appli
2	530.6	31.7	3778	7 US-10-376-763A-5	Sequence 5, Appli
3	312.8	18.7	7794	10 US-11-057-062-2	Sequence 2, Appli
4	310	18.5	10846	3 US-09-923-109-5	Sequence 5, Appli
5	310	18.5	10846	6 US-10-164-204-5	Sequence 5, Appli
6	310	18.5	10846	7 US-10-705-430-5	Sequence 5, Appli
7	310	18.5	10900	3 US-09-923-109-6	Sequence 6, Appli
8	310	18.5	10900	6 US-10-164-204-6	Sequence 6, Appli
9	310	18.5	10900	7 US-10-705-430-6	Sequence 6, Appli
10	310	18.5	11606	7 US-10-602-475A-9	Sequence 6, Appli
11	295	17.6	1998	9 US-10-477-240-8	Sequence 8, Appli
12	289	17.3	12304	9 US-10-473-945-5	Sequence 5, Appli
13	289	17.3	12497	9 US-10-473-945-4	Sequence 4, Appli
14	282	16.8	632	5 US-10-015-637-7	Sequence 7, Appli
15	282	16.8	632	10 US-11-148-661-7	Sequence 7, Appli
16	280.2	16.7	5365	9 US-10-839-092-57	Sequence 57, Appli
17	280.2	16.7	7713	7 US-10-668-240-6	Sequence 6, Appli
18	280.2	16.7	7794	10 US-11-057-062-2	Sequence 2, Appli
19	280.2	16.7	8179	7 US-10-668-240-5	Sequence 5, Appli
20	280.2	16.7	8296	10 US-11-057-069-1	Sequence 1, Appli
21	280.2	16.7	8590	10 US-11-057-062-1	Sequence 1, Appli
22	280.2	16.7	10249	6 US-10-198-478-14	Sequence 14, Appli
23	280.2	16.7	10312	6 US-10-198-478-15	Sequence 15, Appli

Sequence 13, Appli  
Sequence 26, Appli  
Sequence 3, Appli  
Sequence 24, Appli  
Sequence 25, Appli  
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Sequence 2, Appli  
Sequence 8, Appli  
Sequence 1, Appli  
Sequence 8, Appli  
Sequence 15, Appli  
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Sequence 12, Appli  
Sequence 1, Appli  
Sequence 386, Appli  
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Sequence 240, Appli  
Sequence 8, Appli  
Sequence 9, Appli  
Sequence 6854, Appli  
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US-10-838-834-12  
US-10-312-841-1  
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US-10-473-126-386  
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US-10-473-126-240  
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US-10-719-993-6854  
US-10-473-126-240

24 280.2 16.7 10339 6 US-10-376-763A-6  
25 278.8 16.6 10603 8 US-10-376-763A-6  
26 278.8 16.6 10603 8 US-10-376-763A-6  
27 271.4 16.2 10575 8 US-10-376-763A-6  
28 271.4 16.2 10575 8 US-10-376-763A-6  
29 271.2 16.2 15490 9 US-10-376-763A-6  
30 246.6 14.7 9382 9 US-10-376-763A-6  
31 245 14.6 562 9 US-10-376-763A-6  
32 245 14.6 562 9 US-10-376-763A-6  
33 236 14.1 474 7 US-10-415-305-8  
34 185.8 11.1 792 7 US-10-415-602-15  
35 154.4 9.2 8056 8 US-10-473-126-386  
36 153.4 9.2 4767 8 US-10-838-834-12  
37 152.6 9.1 3673778 6 US-10-312-841-1  
38 151.8 9.1 3673778 6 US-10-312-841-1  
39 151.4 9.0 8056 8 US-10-473-126-386  
40 149.4 8.9 158001 7 US-10-211-179-11  
41 148.8 8.9 8056 8 US-10-473-126-240  
42 146.2 8.7 11978 3 US-09-792-568-8  
43 146.2 8.7 12438 3 US-09-792-568-8  
44 145.2 8.7 74665 8 US-10-719-993-6854  
45 144.4 8.6 8056 8 US-10-473-126-240

#### ALIGNMENTS

RESULT 1

US-10-376-763A-6  
; Sequence 6, Application US/10376763A  
; Publication No. US20040172669A1

; GENERAL INFORMATION:  
; APPLICANT: KWS SAAT AG

; TITLE OF INVENTION: Glycosylate tolerant sugar beet

; FILE REFERENCE: KWS-H7-1

; CURRENT APPLICATION NUMBER: US/10/376,763A

; CURRENT FILING DATE: 2003-02-28

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 6

; LENGTH: 3706

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: PCR product

US-10-376-763A-6

Query Match 31.7%; Score 530.6; DB 7; Length 3706;  
Best Local Similarity 92.9%; Pred. No. 1.4e-54;  
Matches 592; Conservative 0; Mismatches 9; Indels 36; Gaps 2;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGTACCATTTATGCTTATCTACTA 60  
DB 3032 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGTACCATTTATGCTTATCTACTA 3091

QY 61 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTTACTGTAACAAGTAGTC 120  
DB 3092 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTTACTGTAACAAGTAGTC 3151

QY 121 CTCTGTGTTTTAGACATTTATGAATCTTCTTTATGTAATTTTCCAGAACTCTTGTGTCAG 180  
DB 3152 CTCTGTGTTTTAGACATTTATGAATCTTCTTTATGTAATTTTCCAGAACTCTTGTGTCAG 3211

QY 181 ATTCTAATCATTCCTTTTATTAATTTATGTTATATCTCATGGATTTGTAGTTAGTATGAAAA 240  
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QY 241 TATTTTTTAATGCATTTTATGATCTCCCAATTCATTTGACCAACATGCATCAATCGACCTGC 300  
DB 3272 TATTTTTTAATGCATTTTATGATCTCCCAATTCATTTGACCAACATGCATCAATCGACCTGC 3331

QY 301 AGCCACTCGAGTGG-----AGGCGCTCATCT 325

Db 3332 AGCCACTCGAAGCGGCGCCACTCGAGTGGTGGCCCGCATCGATCGTGAAGTTTCTCATCT 3391  
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Qy 326 AAGCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 385  
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Db 3392 AAGCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 3451  
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Qy 386 TTTGTTTATTTGCTTTTCGCTTATAAATACGACGGATCGTAATTTGTCGTTTATCAAAATG 445  
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Db 3452 TTTGTTTATTTGCTTTTCGCTTATAAATACGACGGATCGTAATTTGTCGTTTATCAAAATG 3511  
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Qy 446 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTTCGAATTTGAAAAAAATTTGGT 505  
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Db 3512 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTTCGAATTTGAAAAAAATTTGGT 3570  
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Qy 506 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCATGTAGATTT 565  
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Db 3571 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCATGTAGATTT 3630  
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Qy 566 CCGGACATGAGCCATTTACAAATGAATATATTA 602  
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Db 3631 CCGGACATGAGCCATTTACAAATGAATATATCCTA 3667  
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RESULT 2  
US-10-376-763A-5  
; Sequence 5, Application US/10376763A  
; Publication No. US20040172669A1  
; GENERAL INFORMATION:  
; APPLICANT: KWS SAAT AG  
; TITLE OF INVENTION: Glyphosate tolerant sugar beet  
; FILE REFERENCE: KWS-H7-1  
; CURRENT APPLICATION NUMBER: US/10/376,763A  
; CURRENT FILING DATE: 2003-02-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 3778  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Inserted DNA with 3' and 5' flanking sequences  
US-10-376-763A-5

Query Match 31.7%; Score 530.6; DB 7; Length 3778;  
Best Local Similarity 92.9%; Pred. No. 1.4e-54;  
Matches 592; Conservative 0; Mismatches 9; Indels 36; Gaps 2;  
Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTTAGTTGTACCATTTATGCTTATTCACCTA 60  
Db 3077 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTTAGTTGTACCATTTATGCTTATTCACCTA 3136  
Qy 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGTATGTC 120  
Db 3137 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGTATGTC 3196  
Qy 121 CTCCTGTGTTTATAGACATTTATGAACTTTCTTTATGTAATTTTCCAGAATCCTTGTCTAG 180  
Db 3197 CTCCTGTGTTTATAGACATTTATGAACTTTCTTTATGTAATTTTCCAGAATCCTTGTCTAG 3256  
Qy 181 ATTCTAATCATTCCTTTATTAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 240  
Db 3257 ATTCTAATCATTCCTTTATTAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 3316  
Qy 241 TATTTTAAATGATTTTATGACTTCCCAATTTGACAAACATGCAATCAATCGACTGC 300  
Db 3317 TATTTTAAATGATTTTATGACTTCCCAATTTGACAAACATGCAATCAATCGACTGC 3376  
Qy 301 AGCCACTCGAGTGG-----AGGCCTCATCT 325  
Db 3377 AGCCACTCGAAGCGGCGCCACTCGAGTGGTGGCCCGCATCGATCGTGAAGTTTCTCATCT 3436

Qy 326 AAGCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 385  
Db 3437 AAGCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 3496  
Qy 386 TTTGTTTATTTGCTTTTCGCTTATAAATACGACGGATCGTAATTTGTCGTTTATCAAAATG 445  
Db 3497 TTTGTTTATTTGCTTTTCGCTTATAAATACGACGGATCGTAATTTGTCGTTTATCAAAATG 3556  
Qy 446 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTTCGAATTTGAAAAAAATTTGGT 505  
Db 3557 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTTCGAATTTGAAAAAAATTTGGT 3615  
Qy 506 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCATGTAGATTT 565  
Db 3616 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCATGTAGATTT 3675  
Qy 566 CCGGACATGAGCCATTTACAAATGAATATATTA 602  
Db 3676 CCGGACATGAGCCATTTACAAATGAATATATCCTA 3712  
|||||

RESULT 3  
US-11-057-062-2/c  
; Sequence 2, Application US/11057062  
; Publication No. US20050176670A1  
; GENERAL INFORMATION:  
; APPLICANT: Malvar, Thomas  
; APPLICANT: Huang, Shihshieh  
; APPLICANT: Luethy, Michael  
; TITLE OF INVENTION: Recombinant DNA for Gene Suppression  
; FILE REFERENCE: 38-15 (53428)B  
; CURRENT APPLICATION NUMBER: US/11/057,062  
; CURRENT FILING DATE: 2005-02-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 7794  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: recombinant DNA construct in plasmid between Agrobacterium  
; OTHER INFORMATION: borders  
US-11-057-062-2

Query Match 18.7%; Score 312.8; DB 10; Length 7794;  
Best Local Similarity 96.4%; Pred. No. 2.1e-28;  
Matches 320; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTTAGTTGTACCATTTATGCTTATTCACCTA 60  
Db 4040 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTTAGTTGTACCATTTATGCTTATTCACCTA 3981  
Qy 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGTATGTC 120  
Db 3980 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGTATGTC 3921  
Qy 121 CTCCTGTGTTTATAGACATTTATGAACTTTCTTTATGTAATTTTCCAGAATCCTTGTCTAG 180  
Db 3920 CTCCTGTGTTTATAGACATTTATGAACTTTCTTTATGTAATTTTCCAGAATCCTTGTCTAG 3861  
Qy 181 ATTCTAATCATTCCTTTATTAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 240  
Db 3860 ATTCTAATCATTCCTTTATTAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 3801  
Qy 241 TATTTTAAATGATTTTATGACTTCCCAATTTGACAAACATGCAATCAATCGACTGC 300  
Db 3800 TATTTTAAATGATTTTATGACTTCCCAATTTGACAAACATGCAATCAATCGACTGC 3741  
Qy 301 AGCCACTCGAGTGGAGGCGCTCATCTAAGCCCC 332  
Db 3740 AGCCACTCGAAGCGGCGGCTTAAATTAAGGCGC 3709  
|||||





Db 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTATGCTTATTCACTA 2118  
QY 61 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120  
Db 2119 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 2178  
QY 121 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180  
Db 2179 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 2238  
QY 181 ATCTAATCATTCCTTTTAAATATATAGTTATATCTCATGATTTGTTAGTTGAGTATGAAA 240  
Db 2239 ATCTAATCATTCCTTTTAAATATATAGTTATATCTCATGATTTGTTAGTTGAGTATGAAA 2298  
QY 241 TATTTTTTAATGCATTTTATGACTTGCCTTATGTAATTTGTAATTTTCCAGAAATCCTTGTCTAG 300  
Db 2299 TATTTTTTAATGCATTTTATGACTTGCCTTATGTAATTTGTAATTTTCCAGAAATCCTTGTCTAG 2358  
QY 301 AGCCACTCGA 310  
Db 2359 AGCCACTCGA 2368

RESULT 9  
US-10-705-430-6  
; Sequence 6, Application US/10705430  
; Publication No. US20040073976A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard  
; APPLICANT: Keikh, Nordin  
; APPLICANT: Kishore, Ganesh  
; TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 11899 0086 CNUS03 (MOBT:086-3)  
; CURRENT APPLICATION NUMBER: US/10705,430  
; PRIOR FILING DATE: 2003-11-11  
; PRIOR APPLICATION NUMBER: 10/164,204  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: 09/098,219  
; PRIOR FILING DATE: 1998-06-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 6  
; LENGTH: 10900  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: P-FMV/CTP2/Eda/NO3'  
US-10-705-430-6

Query Match 18.5%; Score 310; DB 7; Length 10900;  
Best Local Similarity 100.0%; Pred. No. 4.8e-28;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTATGCTTATTCACTA 60  
Db 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTATGCTTATTCACTA 2118  
QY 61 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120  
Db 2119 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 2178  
QY 121 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180  
Db 2179 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 2238  
QY 181 ATCTAATCATTCCTTTTAAATATATAGTTATATCTCATGATTTGTTAGTTGAGTATGAAA 240  
Db 2239 ATCTAATCATTCCTTTTAAATATATAGTTATATCTCATGATTTGTTAGTTGAGTATGAAA 2298  
QY 241 TATTTTTTAATGCATTTTATGACTTGCCTTATGTAATTTGTAATTTTCCAGAAATCCTTGTCTAG 300

Db 2299 TATTTTTTAATGCATTTTATGACTTGCCTTATGTAATTTGTAATTTTCCAGAAATCCTTGTCTAG 2358  
QY 301 AGCCACTCGA 310  
Db 2359 AGCCACTCGA 2368  
RESULT 10  
US-10-602-475A-9  
; Sequence 9, Application US/10602475A  
; Publication No. US20040128719A1  
; GENERAL INFORMATION:  
; APPLICANT: Klee, Harry J.  
; APPLICANT: Lashbrook, Coralie  
; APPLICANT: Shrode, Lori  
; TITLE OF INVENTION: Materials and Methods for Tissue-Specific Targeting of Ethylene  
; TITLE OF INVENTION: Insensitivity in Transgenic Plants  
; FILE REFERENCE: UF-325XCI  
; CURRENT APPLICATION NUMBER: US/10/602,475A  
; PRIOR FILING DATE: 2003-06-23  
; PRIOR APPLICATION NUMBER: US 60/390,385  
; PRIOR FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 9  
; LENGTH: 11606  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: plasmid construct encoding mutant ethylene receptor  
; NAME/KEY: CDS  
; LOCATION: (1674)..(3890)  
US-10-602-475A-9

Query Match 18.5%; Score 310; DB 7; Length 11606;  
Best Local Similarity 100.0%; Pred. No. 4.9e-28;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTATGCTTATTCACTA 60  
Db 4248 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTTGACCATTATGCTTATTCACTA 4307  
QY 61 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120  
Db 4308 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 4367  
QY 121 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180  
Db 4368 CTCCTGTGTTTATAGACATTTATGAACCTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 4427  
QY 181 ATCTAATCATTCCTTTTAAATATATAGTTATATCTCATGATTTGTTAGTTGAGTATGAAA 240  
Db 4428 ATCTAATCATTCCTTTTAAATATATAGTTATATCTCATGATTTGTTAGTTGAGTATGAAA 4487  
QY 241 TATTTTTTAATGCATTTTATGACTTGCCTTATGTAATTTGTAATTTTCCAGAAATCCTTGTCTAG 300  
Db 4488 TATTTTTTAATGCATTTTATGACTTGCCTTATGTAATTTGTAATTTTCCAGAAATCCTTGTCTAG 4547  
QY 301 AGCCACTCGA 310  
Db 4548 AGCCACTCGA 4557

RESULT 11  
US-10-477-240-8  
; Sequence 8, Application US/10477240  
; Publication No. US20050125862A1  
; GENERAL INFORMATION:  
; APPLICANT: Polston, Jane E.  
; APPLICANT: Hiebert, Ernest  
; TITLE OF INVENTION: Materials and Methods for Producing Tomato Yellow Leaf Curl Virus  
; TITLE OF INVENTION: Resistance in Plants

; FILE REFERENCE: POL-100XCI  
; CURRENT APPLICATION NUMBER: US/10/477,240  
; PRIOR FILING DATE: 2003-11-06  
; PRIOR APPLICATION NUMBER: US 60/289,315  
; PRIOR FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1998  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Expression vector  
US-10-477-240-8

Query Match 17.6%; Score 295; DB 9; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 2.2e-26;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 60  
DB 1703 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 1762  
QY 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 120  
DB 1763 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 1822  
QY 121 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 180  
DB 1823 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 1882  
QY 181 ATTCTAATCATTCCTTTATTAATTTATGTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 240  
DB 1883 ATTCTAATCATTCCTTTATTAATTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 1942  
QY 241 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATCGA 295  
DB 1943 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATCGA 1997

RESULT 12  
US-10-473-945-5  
; Sequence 5, Application US/10473945  
; Publication No. US20050081268A1  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: Kay, Steve A.  
; APPLICANT: Kuhlmann, Tina  
; TITLE OF INVENTION: BIOLUMINESCENT PLANTS AND METHODS OF MAKING SAME  
; FILE REFERENCE: SCRIPT340-1  
; CURRENT APPLICATION NUMBER: US/10/473,945  
; PRIOR FILING DATE: 2003-10-03  
; PRIOR APPLICATION NUMBER: PCT/US02/11116  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 12304  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: ACT-OM-LUC Vector  
US-10-473-945-5

Query Match 17.3%; Score 289; DB 9; Length 12304;  
Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 60  
DB 1703 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 1762  
QY 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 120  
DB 1763 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 1822  
QY 121 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 180  
DB 1823 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 1882  
QY 181 ATTCTAATCATTCCTTTATTAATTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 240  
DB 1883 ATTCTAATCATTCCTTTATTAATTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 1942  
QY 241 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATCGA 295  
DB 1943 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATCGA 1997

DB 3280 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 3339  
QY 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 120  
DB 3340 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 3399  
QY 121 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 180  
DB 3400 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 3459  
QY 181 ATTCTAATCATTCCTTTATTAATTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 240  
DB 3460 ATTCTAATCATTCCTTTATTAATTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 3519  
QY 241 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATC 289  
DB 3520 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATC 3568

RESULT 13  
US-10-473-945-4/c  
; Sequence 4, Application US/10473945  
; Publication No. US20050081268A1  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: Kay, Steve A.  
; APPLICANT: Kuhlmann, Tina  
; TITLE OF INVENTION: BIOLUMINESCENT PLANTS AND METHODS OF MAKING SAME  
; FILE REFERENCE: SCRIPT340-1  
; CURRENT APPLICATION NUMBER: US/10/473,945  
; PRIOR FILING DATE: 2003-10-03  
; PRIOR APPLICATION NUMBER: PCT/US02/11116  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 12497  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: MT-OM-LUC Vector  
US-10-473-945-4

Query Match 17.3%; Score 289; DB 9; Length 12497;  
Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 60  
DB 8630 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 8571  
QY 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 120  
DB 8570 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAATACAAAGTATGTC 8511  
QY 121 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 180  
DB 8510 CTCCTGTGTTTATGACATTTATGAACCTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTCAG 8451  
QY 181 ATTCTAATCATTCCTTTATTAATTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 240  
DB 8450 ATTCTAATCATTCCTTTATTAATTTATGTTTACTCATGATTTGTTAGTTAGTATGAAA 8391  
QY 241 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATC 289  
DB 8390 TATTTTAAATGCAATTTATGACTTGCCTTCCCAATTTGATTGACAAATGATGCAATGCATC 8342

RESULT 14  
US-10-015-637-7



; Sequence 7, Application US/10015637  
; Publication No. US20030046727A1

## GENERAL INFORMATION:

; APPLICANT: Wang, Qi  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Liang, Jihong  
; APPLICANT: Oulmassov, Tim  
; TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof  
; FILE REFERENCE: 13587.106  
; CURRENT APPLICATION NUMBER: US/10/015,637  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: US 60/255879  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7

; LENGTH: 632

; TYPE: DNA

; ORGANISM: Pisum sp.

US-10-015-637-7

Query Match 16.8%; Score 282; DB 5; Length 632;  
Best Local Similarity 100.0%; Pred. No. 6.5e-25;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 60  
DB 351 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 410  
QY 61 GGCAACAATATATTTTTCAGACCTTAGAAAAGCTGCAAAATGTTACTGAAATACAAAGTATGTC 120  
DB 411 GGCAACAATATATTTTTCAGACCTTAGAAAAGCTGCAAAATGTTACTGAAATACAAAGTATGTC 470  
QY 121 CTCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180  
DB 471 CTCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 530  
QY 181 ATTCTAATCATTCCTTTTATATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 240  
DB 531 ATTCTAATCATTCCTTTTATATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 590  
QY 241 TATTTTAAATGCAATTTTATGACTTGCCAAATGATTGACAAC 282  
DB 591 TATTTTAAATGCAATTTTATGACTTGCCAAATGATTGACAAC 632

## RESULT 15

US-11-148-661-7

; Sequence 7, Application US/11148661  
; Publication No. US20050241018A1

## GENERAL INFORMATION:

; APPLICANT: Wang, Qi  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Liang, Jihong  
; APPLICANT: Oulmassov, Tim  
; TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof  
; FILE REFERENCE: 13587.106  
; CURRENT APPLICATION NUMBER: US/11/148,661  
; CURRENT FILING DATE: 2005-06-09  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: US/10/015,637  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: US 60/255879  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7

; LENGTH: 632

; TYPE: DNA

; ORGANISM: Pisum sp.

US-11-148-661-7

Query Match 16.8%; Score 282; DB 10; Length 632;  
Best Local Similarity 100.0%; Pred. No. 6.5e-25;

Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 60  
DB 351 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 410  
QY 61 GGCAACAATATATTTTTCAGACCTTAGAAAAGCTGCAAAATGTTACTGAAATACAAAGTATGTC 120  
DB 411 GGCAACAATATATTTTTCAGACCTTAGAAAAGCTGCAAAATGTTACTGAAATACAAAGTATGTC 470  
QY 121 CTCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180  
DB 471 CTCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 530  
QY 181 ATTCTAATCATTCCTTTTATATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 240  
DB 531 ATTCTAATCATTCCTTTTATATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 590  
QY 241 TATTTTAAATGCAATTTTATGACTTGCCAAATGATTGACAAC 282  
DB 591 TATTTTAAATGCAATTTTATGACTTGCCAAATGATTGACAAC 632

Search completed: March 31, 2006, 07:57:38

Job time : 1291.41 secs

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OM nucleic - nucleic search, using sw model  
Run on: March 31, 2006, 06:18:22 ; Search time 99,926 Seconds  
(without alignments)  
11377.109 Million cell updates/sec

Title: US-10-541-346-2  
Perfect score: 20  
Sequence: 1 ttgaatatattacaagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

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2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

#### ALIGNMENTS

RESULT 1  
CQ860279  
LOCUS CQ860279  
DEFINITION Sequence 2 from Patent WO2004072235.  
ACCESSION CQ860279  
VERSION CQ860279.1  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Cerry,R.E., Duong,C., Hart,J.L., Huber,S.A., Krieb,R.L.,  
Listello,J.J., Martens,A.B. and Sammons,B.  
TITLE Cotton event mon 88913 and compositions and methods for  
detection thereof  
JOURNAL Patent: WO 2004072235-A 2 26-AUG-2004;  
Monsanto Technology LLC (US)  
FEATURES  
source  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Chimeric DNA of cotton genomic DNA and transgene  
insert DNA"

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. NO. 4.2e-03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATACAAAGC 20  
Db 1 TTGAATATATATACAAAGC 20

RESULT 2  
CQ860281  
LOCUS CQ860281  
DEFINITION Sequence 4 from Patent WO2004072235.  
ACCESSION CQ860281  
VERSION CQ860281.1

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	CQ860279 Sequence
2	20	100.0	1675	6	CQ860281 Sequence
3	20	100.0	110000	15	AP008207_139 Continuation (140
4	20	100.0	151041	15	AP003258 Oryza sat
5	20	100.0	207782	15	AP003764 Oryza sat
6	19	95.0	143780	14	AC130943 Rattus no
7	19	95.0	146469	14	AL355991 Homo sapi
8	19	95.0	170141	14	AL611928 Homo sapi
9	19	95.0	171656	8	AL136380 Human DNA
10	19	95.0	177264	9	AL626782 Mouse DNA
11	19	95.0	215043	14	AC094221 Rattus no
12	19	95.0	225692	14	AC125367 Rattus no
13	19	95.0	281699	14	AC127711 Rattus no
14	18.4	92.0	592	10	BV373314 S21P6596
15	18.4	92.0	606	10	BV595271 S21P6122
16	18.4	92.0	754	10	BV472141 G591P6181
17	18.4	92.0	757	10	BV477181 G591P6408
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KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
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AUTHORS Cerny,R.E., Duong,C., Hart,J.L., Huber,S.A., Krieb,R.L.,  
Listello,J.J., Martens,A.B. and Sammons,B.  
TITLE Cotton event mon 88913 and compositions and methods for  
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JOURNAL Patent: WO 2004072235-A 4 26-AUG-2004;  
Monsanto Technology LLC (US)  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Query Match 100.0%; Score 20; DB 15; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20
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RESULT 4
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone:P0463A02.
ACCESSION
AP003258 BA000010
VERSION
AP003258.3 GI:20160658
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1
Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,
Antonilo, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arica, K.,
Hanada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,
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Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J.H., Kim, H.I., Eun, M.Y.,
Yano, M., Jiang, J. and Gojobori, T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
12447438
TITLE
JOURNAL
PUBMED
2 (bases 1 to 151041)
REFERENCE
Sasaki, T., Matsumoto, T. and Yamamoto, K.
AUTHORS
Direct Submission
TITLE
JOURNAL
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
On Apr 16, 2002 this sequence version replaced gi:15146361.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://www.tigr.org/tdb/glimmerm/glmr form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein
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database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0463A02 clone has an overlap with B1051E10 (DDBJ: AP003764) clone at 5' end and with B1102E12 (DDBJ: AF003369) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20

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Db 3308 TTGAATATATATTACAAAGC 3327

## RESULT 5

## AP003764

## LOCUS

## DEFINITION

Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,

BAC clone: B1051E10.

ACCESSION AP003764 BA000010

VERSION AP003764.3 GI:21104808

## KEYWORDS

## SOURCE

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

## AUTHORS

Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,  
Katayose, Y., Wu, J., Nimura, Y., Cheng, Z., Nagamura, Y.,  
Antonio, B. A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,  
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Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukuwa, K.,  
Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,  
Yano, M., Jiang, J., and Gojobori, T.  
The genome sequence and structure of rice chromosome 1

Nature 420 (6913), 312-316 (2002)

12447438

2 (bases 1 to 207782)

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Submitted (20-JUN-2001) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,

Tel: 81-298-38-7441, Fax: 81-298-38-7468)

On May 22, 2002 this sequence version replaced gi:14625024.

Genes were predicted from the integrated results of the following:

GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH

(http://www.softberry.com/), GeneMark.hmm

(http://opal.biology.gatech.edu/GeneMark/), GlimmerM

(http://www.tigr.org/tdb/glimmerm/glmr form.html), RiceHMM

(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor

(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://globin.cse.psu.edu/html/docs/sim4.html), gap2

(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The

genomic sequence was searched against NCBI Nonredundant Protein

database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA

sequence database at RGP or DDBJ. Protein homologies of the coding

regions were searched against NCBI Nonredundant Protein database

with BLASTP. ESTs represent the identified cDNA sequences using

BLASTN with the corresponding DDBJ accession no. and RGP clone ID.

Full-length cDNAs represent the identified cDNA sequences using

BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of B1051E10 clone has an overlap with P0440D10 (DDBJ: AP003852) clone at 5' end and with P0463A02 (DDBJ: AP003258) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/Genomeseq.html>.

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/product="putative SAG12 protein"  
/protein\_id="BAB93394.1"  
/db\_xref="GI:21104809"  
translation="MASSKPLLLGLLSITCLQLVLAANPQPPPPSCDKSKELR  
FMFSOMAKYAKHSCPEQEKRYOVWKGNTNFIGAFRSOTOLSGVGAFAPQITDS  
VVGWNRGDLSTFEVQOFTGFNAGFHSPPPTPLSPHSMOPCCVDMWSGAVGTGKF  
QONCASWAPASAAIEGLHKIKTGEIVLSLEQWVNDCTDSFGSGSHSDPALNLVA  
SRGCTSEKYPYTGVCQSCDVKGLLFDHSASVGFAAVPPNDERQLALAVARQPTV  
YIDASAQFQYKGVKGYPCNPGSNHATVIVGYCENFGGKTYIAKNWSNDWGEQ  
GYVLAKDWWPQGTGCLATSPFYPTV"  
Join(5131..6135,18994..19986)  
/gene="B1051E10.2"  
Join(5131..6135,18994..19986)  
/note="probably inactive due to insertion of genes in CDS  
pseudogene, RIM2 protein"  
/pseudo  
Join(7798..9059,9459..11034)  
/gene="B1051E10.3"  
Join(7798..9059,9459..11034)  
/gene="B1051E10.3"  
/note="putative orf3 of RIRE2"  
complement(11679..14729)  
/gene="B1051E10.4"  
complement(11679..14729)  
/note="probably inactive due to no initiation codon in CDS  
pseudogene, polyprotein"  
/pseudo  
complement(15405..17171)  
/gene="B1051E10.5"  
complement(15405..17171)  
/gene="B1051E10.5"  
/note="probably inactive due to 5' exon missing in CDS  
pseudogene, GAG-POL precursor"  
/pseudo  
complement(20778..21409)  
/gene="B1051E10.6"  
complement(join(<20778..20839,20980..>21409))

```
/gene="B1051E10.6"
/notes="start and end point are not identified"
complement(join(20776..20839,20980..21409))
/gene="B1051E10.6"
/notes="predicted by FGENSEH etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD53838.1"
/db_xref="GI:53792804"
/translation="MDGRRQTHEGGDGGGGEVEAAVVEMATERVAVGDGPVGEV
KAAGVDPGVGEVGVGGVLDLRTAERTSGGGEVGGEGGREGGQRWRGEVE
VGVGEGDGGGEGGEVEAATERRAERRRGRWRWRGREGSAVTGVTCDGLTVRA
RHR"
gene
  join(21457..21569,22350..22440)
  /gene="B1051E10.7"
  join(21457..21569,22350..22440)
misc_feature
  /gene="B1051E10.7"
  /note="hypothetical ORF
  predicted by GlimmerM
  this category is not included in IRGSP standard"
gene
  join(22943..23072,23161..23208,23291..23895,23973..24434,
  24610..25340,25423..25575,25673..25952,26371..26454,
  26869..26925)
  /gene="B1051E10.8"
  join(22943..23072,23161..23208,23291..23895,23973..24434,
  24610..25340,25423..25575,25673..25952,26371..26454,
  26869..26925)
  /gene="B1051E10.8"
  /note="transposon protein-like"
  complement(28374..28924)
  /gene="B1051E10.9"
  complement(join(28374..28465,28581..28650,28769..28924))
  /gene="B1051E10.9"
  /note="start and end point are not identified"
  complement(join(28374..28465,28581..28650,28769..28924))
  /gene="B1051E10.9"
  /note="predicted by GeneMark.hmm etc."
  /codon_start=1
  /product="hypothetical protein"
  /protein_id="BAD53839.1"
  /db_xref="GI:53792805"
  /translation="MATVSQKLGDCGCSAQAGHQRGRRRHGRISAVARELVRAVD
  LDPSTQTLCMIVAAATTRFKADNFGPMFIPVDIVGSKLDMEDHLFTSTPIHSSS
  GHY"
gene
  30450..36329
  /gene="B1051E10.10"
  join(30450..30774,31708..31779,31905..31970,32069..32125,
  32219..32286,32370..32451,32747..32802,32947..33249,
  33344..33430,33501..33675,33783..33904,33991..34154,
  34227..34481,34614..34735,34844..34965,35413..35561,
  35648..35786,36017..36329)
  /gene="B1051E10.10"
  /note="supported by full-length cDNA(s): AK100444"
  join(30666..30774,31708..31779,31905..31970,32069..32125,
  32219..32286,32370..32451,32747..32802,32947..33249,
  33344..33430,33501..33675,33783..33904,33991..34154,
  34227..34481,34614..34735,34844..34965,35413..35561,
  35648..35786,36017..36052)
  /gene="B1051E10.10"
  /note="contains EST(s): AU063400 (C61341), AU085835 (C61341)
  contains full-length cDNA(s): AK100444, AK062168, AK099063"
  /codon_start=1
  /product="putative tetrafunctional protein of glyoxysomal
  fatty acid beta-oxidation"
  /protein_id="BAB93398.1"
  /db_xref="GI:21104813"
  /translation="WAAAAAKGTEMEVGADGVAVITICNPVNSLSIDVLSIKEN
  YAEALRRNDVAIVTGGKFGSGFDISSFGSVGGKVEQPKVGYISIDITITLEA
  AKTSVAIDGLGGEVAVACHARISTPTAQGLPELQVPGVIGGQRLPRLV
  GLTKALEMLGSKPIKGAHQGLVDLSADLVNTRWALDIDCELPKPIKSLY
  KTDKLEPLGEAREILKFARAQRQAANLEHPLVICIDVIEEGIVSGFAGLWKEANAF
```

Query Match

100.0%; Score 20; DB 15; Length 207782;

```
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAGC 20
|||||
Db 87865 TTGAATATATATTACAAGC 87884

RESULT 6
AC130943 143780 bp DNA linear HTG 20-NOV-2002
LOCUS Rattus norvegicus clone CH230-410L18, *** SEQUENCING IN PROGRESS
DEFINITION ***
AC130943
AC130943.3 GI:25138999
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus;
Muzny,D,Marie., Metzker,M,Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gunaratne,P., Haaland,W., Hamil,C., Henderson,N., Hernandez,J.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hamilton,K.,
Hollands,B., Howells,S., Hladun,S.L., Hodgson,A., Hognes,M.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaeleleleh,O., Okwunolu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pul.L., Reigh,R.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savory,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D.,
Sneed,J., Sodergren,B., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu.F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
TITLE
JOURNAL
Unpublished
```



```

REFERENCE
AUTHORS      2 (bases 1 to 143780)
TITLE        Rat Genome Sequencing Consortium.
JOURNAL      Direct Submission
Submitted (15-AUG-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
REFERENCE
AUTHORS      3 (bases 1 to 143780)
TITLE        Rat Genome Sequencing Consortium.
JOURNAL      Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT
On Nov 20, 2002 this sequence version replaced gi:23908408.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KCAT
Center clone name: CH230-410L18
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 133773 bases at least Q40
Consensus quality: 135099 bases at least Q30
Consensus quality: 135971 bases at least Q20
Estimated insert size: 137896; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 143780: contig of 143780 bp in length.
Location/Qualifiers
1 .143780
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-410L18"
1 .1037
/notes="wgs_end_extension
clone_end:T7"
clone_end:T7
/notes="wgs_end_extension
clone_end:T7"
clone_end:T7
/notes="clone_boundary
clone_end:T7"
site:
end_sequence:BZ116678"
132383. .13539
/notes="clone boundary
clone_end:Sp6"

FEATURES
source
1 .143780
misc_feature
1 .1037
misc_feature
2707..3905
misc_feature
6327..7277
misc_feature
132383..13539

```

```

site:
end_sequence:BZ116680"
134792. .136777
/notes="wgs_end_extension
clone_end:Sp6"
137952. .140046
/notes="wgs_end_extension
clone_end:Sp6"
141598. .143780
/notes="wgs_end_extension
clone_end:Sp6"

misc_feature
134792..136777
misc_feature
137952..140046
misc_feature
141598..143780

ORIGIN
Query Match 95.0%; Score 19; DB 14; Length 143780;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGAATATATATATTACAAAGC 20
|||||
Db 50434 TGAATATATATATTACAAAGC 50452

RESULT 7
AL355991 146469 bp DNA linear HTG 10-JUL-2001
LOCUS AL355991 Homo sapiens chromosome 1 clone RP11-149G23, 22 unordered pieces.
DEFINITION AL355991 AC026255
ACCESSION AL355991.5 GI:9800917
VERSION HTG; HTGS_PHASE1; HTGS_CANCELLED.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Plumb,B.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT
On or before May 15, 2001 this sequence version replaced
gi:10280883, gi:9213695.
Draft Sequence Produced by Whitehead Institute/MIT Center for
Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA
http://www-seq.wi.mit.edu
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bA149G23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 138717 bases at least Q40
Consensus quality: 14163 bases at least Q30
Consensus quality: 142550 bases at least Q20
Insert size: 144369; sum-of-contigs
Insert size: 180875; 7.0% error; agarose-fp
Quality coverage: 3.80x in Q20 bases; sum-of-contigs Quality
coverage: 3.19x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 4659: contig of 4659 bp in length
* 4660 4759: gap of 100 bp
* 4760 10177: contig of 5418 bp in length
* 10178 10277: gap of 100 bp
* 10278 13628: contig of 3351 bp in length
* 13629 13728: gap of 100 bp
* 13729 15928: contig of 2200 bp in length
* 15929 16028: gap of 100 bp
* 16029 21103: contig of 5075 bp in length
* 21104 22003: gap of 100 bp
* 22004 26013: contig of 4810 bp in length
* 26014 26113: gap of 100 bp
* 26114 28336: contig of 2223 bp in length
* 28337 28436: gap of 100 bp
* 28437 31764: contig of 3328 bp in length
* 31765 31864: gap of 100 bp
* 31865 43436: contig of 11572 bp in length
* 43437 43536: gap of 100 bp
* 43537 45726: contig of 2190 bp in length
* 45727 45826: gap of 100 bp
* 45827 48850: contig of 4024 bp in length
* 48851 49950: gap of 100 bp
* 49951 83597: contig of 33647 bp in length
* 83598 83697: gap of 100 bp
* 83698 89161: contig of 5464 bp in length
* 89162 89261: gap of 100 bp
* 89262 92494: contig of 3233 bp in length
* 92495 92594: gap of 100 bp
* 92595 97485: contig of 4891 bp in length
* 97486 97585: gap of 100 bp
* 97586 100084: contig of 2499 bp in length
* 100085 100184: gap of 100 bp
* 100185 112061: contig of 11877 bp in length
* 112062 112161: gap of 100 bp
* 112162 117082: contig of 4921 bp in length
* 117083 117182: gap of 100 bp
* 117183 121364: contig of 4182 bp in length
* 121365 121465: gap of 100 bp
* 121465 125730: contig of 4266 bp in length
* 125731 125831: gap of 100 bp
* 125831 129668: contig of 3838 bp in length
* 129669 129768: gap of 100 bp
* 129769 146469: contig of 16701 bp in length.

FEATURES
    source
        1..146469
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="1"
            /clone_lib="RPCI-11.1"
            /clone="RP11-149G23"
            /clone_lib="RPCI-11.1"
            1..4659
                /note="assembly_fragment:01603"
                clone_end:SP6
                vector_side:left
                4760..10177
                    /note="assembly_fragment:00298"
                    fragment_chain:1
                10278..13628
                    /note="assembly_fragment:00832"
                    fragment_chain:1
                13729..15928
                    /note="assembly_fragment:00657"
                    fragment_chain:1
                16029..21103
                    /note="assembly_fragment:00451"
                    fragment_chain:1
                21204..26013
                    /note="assembly_fragment:00964"
                    fragment_chain:1
                26114..28336
                    /note="assembly_fragment:00715"
                    fragment_chain:2

```

```

misc_feature 28437..31764
    /note="assembly_fragment:00592"
    fragment_chain:2
misc_feature 31865..43436
    /note="assembly_fragment:00602"
    fragment_chain:2
misc_feature 43537..45726
    /note="assembly_fragment:01102"
    fragment_chain:3
misc_feature 45827..49850
    /note="assembly_fragment:00532"
    fragment_chain:3
misc_feature 49951..83597
    /note="assembly_fragment:01625"
    fragment_chain:3
misc_feature 83698..89161
    /note="assembly_fragment:00330"
    fragment_chain:4
misc_feature 89262..92494
    /note="assembly_fragment:00141"
    fragment_chain:4
misc_feature 92595..97485
    /note="assembly_fragment:00934"
    fragment_chain:5
misc_feature 97586..100084
    /note="assembly_fragment:00611"
    fragment_chain:5
misc_feature 100185..112061
    /note="assembly_fragment:01069"
    fragment_chain:6
misc_feature 112162..117082
    /note="assembly_fragment:01346"
    fragment_chain:6
misc_feature 117183..121364
    /note="assembly_fragment:00110"
    fragment_chain:6
misc_feature 121465..125730
    /note="assembly_fragment:00294"
    fragment_chain:6
misc_feature 125831..129668
    /note="assembly_fragment:00955"
    fragment_chain:6
misc_feature 129769..146469
    /note="assembly_fragment:00166"
    clone_end:T7
    vector_side:right

ORIGIN
Query Match 95.0%; Score 19; DB 14; Length 146469;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATATATATTTACAAAG 19
    |||||
Db 37702 TTGAATATATATTTACAAAG 37720

RESULT 8
LOCUS AL611928 170141 bp DNA linear HTG 16-NOV-2001
DEFINITION Homo sapiens chromosome 1 clone RP11-102H4, 19 unordered pieces.
ACCESSION AL611928
VERSION AL611928.7 GI:16073747
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1
AUTHORS Phillimore,B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 11, 2001 this sequence version replaced gi:16030263.
COMMENT

```

```
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA157D21
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 156102 bases at least Q40
Consensus quality: 166989 bases at least Q30
Consensus quality: 167607 bases at least Q20
Insert size: 168341; sum-of-contigs
Insert size: 184691; 1.6% error; agarose-fp
Quality coverage: 7.77x in Q20 bases; sum-of-contigs Quality
coverage: 7.49x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 7583: contig of 7583 bp in length
* 7584 7683: gap of 100 bp
* 7684 37643: contig of 29960 bp in length
* 37644 37743: gap of 100 bp
* 37744 44330: contig of 6587 bp in length
* 44331 44430: gap of 100 bp
* 44431 48789: contig of 4359 bp in length
* 48790 48889: gap of 100 bp
* 48890 51359: contig of 2470 bp in length
* 51360 51460: gap of 100 bp
* 51460 68819: contig of 17360 bp in length
* 68820 68919: gap of 100 bp
* 68920 77759: contig of 8740 bp in length
* 77760 80295: contig of 2536 bp in length
* 80296 80396: gap of 100 bp
* 80396 96780: contig of 16385 bp in length
* 96781 96880: gap of 100 bp
* 96881 104833: contig of 7953 bp in length
* 104834 104934: gap of 100 bp
* 104934 107701: contig of 2768 bp in length
* 107702 110156: contig of 2355 bp in length
* 110157 110256: gap of 100 bp
* 110257 114637: contig of 4381 bp in length
* 114638 114738: gap of 100 bp
* 114738 119077: contig of 4340 bp in length
* 119078 119178: gap of 100 bp
* 119178 128680: contig of 9503 bp in length
* 128681 128781: gap of 100 bp
* 128781 137661: contig of 8881 bp in length
* 137662 137762: gap of 100 bp
* 137762 143331: contig of 5570 bp in length
* 143332 143432: gap of 100 bp
* 143432 162121: contig of 18690 bp in length
* 162122 162222: gap of 100 bp
* 162222 170141: contig of 7920 bp in length.
* Location/Qualifiers
* 1..170141
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /chromosome="1"
* /clone="RP11-102H4"
* /clone_lib="RPC1-11.1"
* misc_feature 1..7583
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clone_end:SP6
vector_side:left"
7684..37643
/note="assembly_fragment:00552
fragment_chain:1"
37744..44330
/note="assembly_fragment:02877
fragment_chain:1"
44431..48789
/note="assembly_fragment:03779
fragment_chain:1"
48890..51359
/note="assembly_fragment:02144
fragment_chain:1"
51460..68819
/note="assembly_fragment:00819
fragment_chain:1"
68920..77759
/note="assembly_fragment:01231
fragment_chain:1"
77760..80295
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80396..96780
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96881..104833
/note="assembly_fragment:00628
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104934..107701
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107802..110156
/note="assembly_fragment:02206
fragment_chain:2"
110257..114637
/note="assembly_fragment:00145
fragment_chain:3"
114738..119077
/note="assembly_fragment:02879
fragment_chain:3"
119178..128680
/note="assembly_fragment:01354"
128781..137661
/note="assembly_fragment:04167"
137762..143331
/note="assembly_fragment:03200
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143432..162121
/note="assembly_fragment:03145
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162222..170141
/note="assembly_fragment:00980
fragment_chain:4
clone_end:T7
vector_side:right"
ORIGIN
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Query Match 95.0%; Score 19; DB 14; Length 170141;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TTGAATATATATACAAAG 19
|||||
Db 149141 TTGAATATATATACAAAG 149159
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```
RESULT 9
AL136380
```

```
LOCUS AL136380 171656 bp DNA linear PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone RP5-88207 on chromosome 1p33-34.2
Contains the 5' end of the PTC42 gene for patched homolog 2
```

(Drosophila), a ribosomal protein S2 (RPS2) pseudogene, the EIF2B3 gene for eukaryotic translation initiation factor 2B subunit 3 gamma 58kba, a chromosome 14 open reading frame 18 (C14orf18) pseudogene, a peptidylprolyl isomerase A (cyclophilin A) (PP1A) pseudogene, a mitochondrial ribosomal protein S17 (MRPS17) pseudogene and four CpG islands, complete sequence.

## ACCESSION

AL136380

## VERSION

AL136380.22 GI:19031310

## KEYWORDS

HTG; C14orf18; CpG island; EIF2B3; MRPS17; patched; PP1A; PTCH2;

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 171656)

## AUTHORS

Phillimore, B.

## TITLE

Direct Submission

## JOURNAL

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,

## COMMENT

Clone requests: clonerequest@sanger.ac.uk  
On Feb 28, 2002 this sequence version replaced gi:18857781.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL; Swi, SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr1>

RPS-88207 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

-----

Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>Contact: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)

-----

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

## FEATURES

## source

1..171656  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/map="p33-34.2"  
/clone="RPS-88207"  
/clone\_lib="RPCI-5"  
1  
/note="Clone left end: RPS-88207"  
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complement(AL592166.16:85961..90550))  
/gene="PTCH2"

## misc\_feature

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complement(7630..7819),complement(7453..7522),  
complement(7184..7275),complement(6326..6521),  
complement(5387..5508),complement(5092..5239),  
complement(4880..5011),complement(4635..4790),  
complement(4460..4552),complement(3984..4109),  
complement(3774..3892),complement(3321..3669),  
complement(2880..3192),complement(2645..2787),  
complement(2380..2560),complement(2001..2246),  
complement(AL592166.16:90516..90550),

complement(AL592166.16:90278..90415),  
complement(AL592166.16:87271..87413),  
complement(AL592166.16:87097..87196),  
complement(AL592166.16:85961..86697))  
/gene="PTCH2"  
/locus\_tag="RP11-269F19.8-001"  
/note="patched homolog 2 (Drosophila)"  
/product="patched homolog 2 (Drosophila)"  
/note="match: ESTs: Em:AI853051.1 Em:BE197960.1  
Em:BE234509.1 Em:BG384338.1 Em:BI541783.1 Em:BM105989.1  
Em:BX634936.1 Em:CD548301.1  
match: cDNAs: Em:AF087651.1 Em:AF091501.1 Em:AF119569.1"  
join(Complement(18339..18410),complement(17325..17517),  
complement(7630..7819),complement(7453..7522),  
complement(7184..7275),complement(6326..6521),  
complement(5387..5508),complement(5092..5239),  
complement(4880..5011),complement(4635..4790),  
complement(4460..4552),complement(3984..4109),  
complement(3774..3892),complement(3321..3669),  
complement(2880..3192),complement(2645..2787),  
complement(2380..2560),complement(2001..2246),  
complement(AL592166.16:90516..90550),  
complement(AL592166.16:90278..90415),  
complement(AL592166.16:87271..87413),  
complement(AL592166.16:87097..87196),  
complement(AL592166.16:86443..86697))  
/gene="PTCH2"

## CDS

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/standard\_name="OrthoMPE0000010158"

/note="match: proteins: Sw:Q9Y6C5"

/codon\_start=1

/product="patched homolog 2 (Drosophila)"

/protein\_id="CAI23127.1"

/db\_xref="GI:56204905"

/db\_xref="InterPro:IPR000731"

/db\_xref="InterPro:IPR003392"

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/translation="MTRSPRLRELPSYTPPARTAAPQILAGSLKAPLWLRAYFOGLL  
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KLGEAAATYQMLIQTARQGENILTFEALGLHQALITASKVQVSLYKRGSLDNKIK  
YKSGVPLIENGIMIERMIEKLPFCVILTPDFCWEGAKQGGSAVLPGRPD1QWNLDP  
EQLLEELGPFASLEGFELDKAQGVQYVGRPCVHPDLDLHCPSPAPNHHSRQAPNVA  
HELSSGCHGFSHKFMWQEBLLGGMARDPQGLLRAELASTFLSPRSLYLFHFRG  
DYOTD1GWSEEOASTVLOAWORFVLOAEALPENASQOIHFSS1TDL1LHAFSE  
VSARVVGGVLLMLAYACTWMLWDCAQSGSVGLAGVLLVALAVASGLICALLGIT  
FNAATVVLFLALIGVDVDFLLAHAFALPTALPTQERMGECLORTGTSVLTSLIN  
NMAFLMAALVLPALRAFSLQAAIVVGGCTFVAVLVFPAVLPALLSLDLRRHCCQLDLVC  
CFSPSCSAQVLIQLPQELGDTGVPIAHLTATVQAFTHCEASQHVVTILPQAHLLQ  
PPSPDPLGSELFSPGSTRDLGQEEETROKACKSLFCARWNLAHFARYOFAPLLQ  
SHAKAIVLVLFGALLGLSLYGATLVQDGLATDVVPRGTKEHAFSLAQRLFYSLYEVA  
LVTQCGFDYAHQSORALFDLHORFSSKAVLPPPAQAPRTWLHYRNWLOGLIOAADFQ  
DMASGRITRHSYNGSEDGALAYKLLLTQDGAEPDFDSQLTTRKLVDRGLIPEFLF  
YMGLTWVSSDDPLGLAASQANFYPPPEWLHDKDITTGENLRIPPAQLEFAQPFPLF  
RGLQKTADFVEAIEGARAACAAGQAGHAYPGSGPFLFWEQYLGRLRCFLAVCILL  
VCTFLVCALLLNLPWTAGLIVLVMATMVELFGIMGFLGKLSAIPVVLVASVGIGV  
EFTVHVALGFLTQGSNRNAAHALEHTFAPVTDGASTLGLMLAGSHFDFTVRYF  
FAALTVLTLGLLGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGGSLRWAGS  
SSLPQSPARVTTSTMTVAHPPLPGAIHFAPDEPPWSPATSSGNLSRRGPGATG"  
13103  
/note="Clone right end: RP11-269F19"  
complement(19399..19560)  
/locus\_tag="RPS-88207.1-001"  
/pseudo  
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/locus\_tag="RPS-88207.1-001"  
/note="match: proteins: Sw:O18789 Sw:P15980 Sw:P27952  
Tr:AAGI3953 Tr:AAH02186 Tr:BAB28188 Tr:O55211 Tr:O55212  
Tr:O55214 Tr:Q8N5L9"  
/pseudo  
/codon\_start=1  
/product="ribosomal protein S2 (RPS2) pseudogene"  
/note="match: ribosomal protein S2 (RPS2) pseudogene"  
complement(26254)  
complement(join(26256..26481,33182..33285,50156..50304,  
51096..51173,55296..55486,57090..57217,72833..72922,

## misc\_feature

## gene

## CDS

## polyA\_site

## gene

102106. .102217,116984. .117143,153793. .153938,  
156499. .156655,161971. .162088))  
/gene="EIF2B3"  
/locus\_tag="RP5-88207.2-001"  
complement(join(26256. .26481,33182. .33285,50156. .50304,  
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102106. .102217,116984. .117143,153793. .153938,  
156499. .156655,161971. .162088))  
/gene="EIF2B3"  
/locus\_tag="RP5-88207.2-001"  
/product="eukaryotic translation initiation factor 2B,  
subunit 3 gamma, 58kDa"  
/note="match: ESTs: Em:AI143649.1 Em:AI798535.1  
Em:AUI42843.1 Em:BG196826.1 Em:BG327641.1 Em:BI551191.1  
Em:BI770446.1 Em:BM788768.1 Em:BQ776018.1 Em:BU608183.1  
Em:CA488835.1 Em:CB130475.1 Em:CB218437.1 Em:CD516142.1  
Em:CD520159.1 Em:Z41323.1  
match: cDNAs: Em:AK024006.1"  
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55296. .55486,57090. .57217,72833. .72922,102106. .>102133))  
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/locus\_tag="RP5-88207.2-008"  
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55296. .55486,57090. .57217,72833. .72922,102106. .>102133))  
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subunit 3 gamma, 58kDa"  
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complement(26336. .26341)  
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/locus\_tag="RP5-88207.2-008"  
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156499. .156646))  
/gene="EIF2B3"  
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Tr:Q8AVU8"  
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/product="eukaryotic translation initiation factor 2B,  
subunit 3 gamma, 58kDa"  
/protein\_id="CAI23131.1"  
/db\_xref="GI:56204907"  
/db\_xref="InterPro:IPR005835"  
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Query Match 95.0%; Score 19; DB 8; Length 171656;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAG 19  
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Db 103330 TTGAATATATATTACAAAG 103348

RESULT 10  
AL626782/c  
LOCUS  
DEFINITION Mouse DNA sequence from clone RP23-335N15 on chromosome X, complete  
sequence.  
ACCESSION AL626782  
VERSION AL626782.10 GI:20068573  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciuognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 177264)  
Phillimore,B.  
Direct Submission  
Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humuys@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk  
On Apr 7, 2002 this sequence version replaced gi:19031574.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em: EMBL; Sw:  
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep RP23-335N15 is  
from the RPCI-23 Mouse PAC Library  
constructed by the group of Pieter de Jong.  
For further details see http://www.chori.org/bacpac/home.htm  
VECTOR: pBAC3.6  
----- Genome Center  
Center: UK Medical Research Council  
Center code: UK-MRC  
Web site: http://mrcseq.har.mrc.ac.uk  
Contact: mouse@har.mrc.ac.uk  
-----  
Location/Qualifiers  
1. 177264  
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/db\_xref="taxon:10090"  
/chromosome="X"  
/clone="RP23-335N15"  
/clone\_lib="RPCI-23"

Query Match 95.0%; Score 19; DB 9; Length 177264;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAATATATATTACAAAGC 20  
|||||

Db 100784 TGAATATATATTACAAAGC 100766

RESULT 11  
AC094221/c  
LOCUS  
DEFINITION Rattus norvegicus clone CH230-2P14, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
2 unordered pieces.  
ACCESSION AC094221  
VERSION AC094221.9 GI:30467641  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciuognathi; Muroidea; Muridae; Murinae; Rattus.  
1 (bases 1 to 215043)  
REFERENCE  
AUTHORS Muzny,D,Marie., Metzker,M, Lee., Abranzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,

Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, N., Hughes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebaird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulseged, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, B., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapu, P., Martin, K., Martin, R., Martinez, B., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokedemeh, O., Okwunigbo, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pffannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rokey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savory, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajes, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 215043)  
Worley, K.C.  
Direct Submission  
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 215043)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On May 9, 2003 this sequence version replaced gi:24819444.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GAFN  
Center clone name: CH230-2P14  
----- Summary Statistics  
Assembly program: Atlas;  
Consensus quality: 209974 bases at least Q40  
Consensus quality: 211630 bases at least Q30  
Consensus quality: 212387 bases at least Q20  
Estimated insert size: 224886; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 213195: contig of 213195 bp in length  
\* 213196 213295: gap of unknown length  
\* 213296 215043: contig of 1748 bp in length.  
FEATURES  
source  
1. 215043  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clones="CH230-2P14"  
213196..213295  
/estimated\_length=unknown  
gap  
ORIGIN  
Query Match 95.0%; Score 19; DB 14; Length 215043;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 TGAATATATATATACAAAGC 20  
|||||  
Db 169783 TGAATATATATACAAAGC 169765  
AC125367 225692 bp DNA linear HTG 09-MAY-2003  
AC125367/c  
LOCUS  
DEFINITION Rattus norvegicus clone CH230-4F4, WORKING DRAFT SEQUENCE, 5  
unrounded pieces.  
AC125367  
AC125367.4 GI:30466981  
HTG: HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.  
Rattus norvegicus (Norway rat)  
SOURCE  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 225692)  
Muzny, D., Marle, Metzker, M., Lee, Abramzon, S., Adams, C., Alder, J.,  
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,  
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
Baldwin, B., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,  
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,  
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,  
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, N., Hughes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebaird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulseged, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, B., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapu, P., Martin, K., Martin, R., Martinez, B., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokedemeh, O., Okwunigbo, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pffannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rokey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savory, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajes, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Joliviet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kwis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheva, L., Loulsegged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakoelameh, O., Okwuonu, G., Olarnpunaagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzio, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, R., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished  
2 (bases 1 to 225692)  
Worley, K.C.

Direct Submission  
Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 225692)  
Rat Genome Sequencing Consortium.

Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:22772437.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GAPO

Center clone name: CH230-4F4

----- Summary Statistics

Assembly program: Atlas;  
Consensus quality: 212691 bases at least Q40  
Consensus quality: 215052 bases at least Q30  
Consensus quality: 216903 bases at least Q20  
Estimated insert size: 223398; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 218818: contig of 218818 bp in length  
\* 218819 218918: gap of unknown length  
\* 218919 220130: contig of 1212 bp in length  
\* 220131 220230: gap of unknown length  
\* 220231 221911: contig of 1681 bp in length  
\* 221912 222011: gap of unknown length  
\* 222012 223534: contig of 1523 bp in length  
\* 223535 223634: gap of unknown length  
\* 223635 225692: contig of 2058 bp in length.

## FEATURES

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/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-4F4"

## misc\_feature

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clone end:Sp6  
site:EcoRI  
115825..117279  
end\_sequence:BH306276"

## misc\_feature

/note="wgs contig"  
complement(216935..217818)  
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clone end:T7  
site:EcoRI  
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end\_sequence:BH306274"

## misc\_feature

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complement(216935..217818)  
/note="clone boundary  
clone end:T7  
site:EcoRI  
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end\_sequence:BH306274"

## gap

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## gap

220131..220230  
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## gap

221912..222011  
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## gap

223535..223634  
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## ORIGIN

Query Match 95.0%; Score 19; DB 14; Length 225692;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGAATATATATATACAAAGC 20  
|||||

Db 87925 TGAATATATATATACAAAGC 87907  
|||||

## RESULT 13

AC127711/c

LOCUS

DEFINITION

Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711

AC127711.3

GI:25078806

HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.

AC127711 281699 bp DNA linear HTG 19-NOV-2002  
Rattus norvegicus clone CH230-62C14, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 6 unordered pieces.



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE  
AUTHORS

1 (bases 1 to 281699)  
Murny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Albrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,A., Chacko,J., Chavez,D., Chen,G., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.I., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseghe,H., Lozada,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mahtoney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackemeoh,O., Okwuonu,G., Olaxpungagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,P., Poinexter,A., Popovic,D., Primus,E., Pu.L.-L., Puzo,M., Quiroz,J., Rachin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,M., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE  
JOURNAL

2 (bases 1 to 281699)  
Unpublished  
Worley,K.C.  
Direct Submission  
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS

3 (bases 1 to 281699)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 19, 2002 this sequence version replaced gi:23267553. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GZVR  
Center clone name: CH230-62C14  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 235016 bases at least Q40  
Consensus quality: 239978 bases at least Q30  
Consensus quality: 242716 bases at least Q20  
Estimated insert size: 242699; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation  
-----

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 8443: contig of 8443 bp in length  
8444 8543: gap of unknown length  
8544 261385: contig of 252842 bp in length  
261386 261485: gap of unknown length  
261486 262787: contig of 1302 bp in length  
262788 262887: gap of unknown length  
262888 265014: contig of 2127 bp in length  
265015 265114: gap of unknown length  
265115 268869: contig of 3755 bp in length  
268870 268969: gap of unknown length  
268970 281699: contig of 12730 bp in length.

FEATURES  
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/db\_xref="taxon:10116"  
/clone="CH230-62C14"

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8544. 9701  
/note="wgs contig"

misc\_feature

25995. 261385  
/note="wgs contig"

gap

261386. 261485  
/estimated\_length=unknown

gap

262788. 262887  
/estimated\_length=unknown

gap

265015. 265114  
/estimated\_length=unknown

gap

268870. 268969  
/estimated\_length=unknown

ORIGIN

Query Match 95.0%; Score 19; DB 14; Length 281699;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0;  
Qy 2 TGAATATATATATACAAAGC 20  
|||||  
Db 20568 TGAATATATATATACAAAGC 20550



RESULT 14  
 BV373314  
 LOCUS  
 DEFINITION S231P6596FC11.T0 BedlingtonTerrier Canis familiaris STS 28-JAN-2005  
 sequence tagged site.  
 ACCESSION BV373314  
 VERSION BV373314.1 GI:57627384  
 SOURCE STS.  
 ORGANISM Canis familiaris (dog)  
 Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.  
 REFERENCE 1 (bases 1 to 592)  
 AUTHORS Lindblad-Toh, K.  
 TITLE The genome sequence of Canis familiaris  
 JOURNAL Unpublished (2004)  
 COMMENT

Contact: Kerstin Lindblad-Toh  
 Whitehead Institute for Biomedical Research, Center for Genome  
 Research  
 320 Charles Street, Cambridge, MA 02141, USA  
 Tel: 6172521477  
 Fax: 6172580903  
 Email: kersli@genome.wi.mit.edu  
 Primer A: No sequence submitted  
 Primer B: No sequence submitted  
 STS size: 592

Protocol:  
 WGS-discovery (WGS):  
 Paired-end low-coverage whole genome shotgun reads were generated  
 from 9 breeds  
 (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador  
 Retriever, English  
 Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese  
 Water Dog -100,000 each)  
 and five other canids (Chinese, Alaskan, Indian and Spanish Gray  
 Wolf as well as the  
 Californian Coyote).

The WGS reads were placed uniquely on the CanFam1.0 boxer assembly  
 and SNP detection was  
 carried out by SSAHA-SNP. 863872 reads were annotated as STSs and  
 485941 SNPs were  
 annotated with alleles from the boxer and the breed or canid from  
 which the particular  
 read came. The validation rate for these SNPs was estimated at  
 approximately 98%.

WGA-discovery (WGA) of Boxer/Poodle SNPs:  
 A second set of SNPs was generated using a similar methodology  
 except that the contigs  
 from the 1.5x poodle assembly (Kirkness 2003) were used instead of  
 WGS reads. Since this  
 sequence lacked base quality scores, arbitrary quality scores of  
 phred 40 were assigned  
 before the poodle sequence was placed uniquely on the CanFam1.0  
 boxer assembly and SNP  
 detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated  
 with alleles from the  
 boxer and the poodle. The validation rate for these SNPs was  
 estimated at approximately TBD%.

Internal-WGA-discovery (I-WGA):  
 A third set of SNPs were discovered by comparing reads in the WGA  
 assembly. SNPs were  
 defined as mismatch positions that had a base quality of >= 30 on  
 both reads in a region  
 that aligned without gaps, and with at most one additional mismatch  
 in the ten flanking  
 bases. For each allele, at least one additional read had to confirm  
 it. 731476 SNPs were  
 annotated with alleles between the two boxer alleles. The  
 validation rate for these SNPs

was estimated at approximately TBD%.

FEATURES  
 source

1..592  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="BedlingtonTerrier"  
 /db\_xref="taxon:9615"  
 /map="+" 27 22-544 38436142-38435620"  
 /clone\_lib="BedlingtonTerrier"  
 <1..>592

STS  
 ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 592;  
 Best Local Similarity 95.0%; Pred. No. 4.9e+03;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATACAAAGC 20  
 |||||  
 Db 507 TTGAATCTATATTACAAAGC 526

RESULT 15  
 BV595271

LOCUS  
 DEFINITION

BV595271 606 bp DNA linear STS 14-APR-2005  
 S215P61223RG4.T0 Clara Pan troglodytes troglodytes STS genomic,  
 sequence tagged site.

ACCESSION  
 VERSION

KEYWORDS  
 SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 606)  
 Mikelsen, T.S., Hillier, W.L., Eichler, E.E., Zody, M.C. and  
 Jaife, D.B.  
 Initial Sequence of the Chimpanzee Genome and Comparison with the  
 Human Genome  
 Unpublished (2005)

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 Primer A: No sequence submitted  
 Primer B: No sequence submitted  
 STS size: 606

Protocol:  
 23,021,928 chimpanzee whole genome shotgun reads were aligned to  
 the Human genome NCBI  
 Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,  
 including Clint (Pan  
 troglodytes verus), 3 other Pan troglodytes verus chimps  
 (Donald, Karlien, Yvonne), 3 Pan  
 troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps  
 of unknown origin

(Gon, Unknown Chimp). Common names: Pan troglodytes verus is the  
 western chimp and Pan  
 troglodytes troglodytes is the central chimp. To be included in  
 chimpanzee SNP discovery, a  
 read must be at least 500bp in length, at least 50% of its base  
 calls must have Phred  
 score >= 20, at least 30% of its base calls must satisfy  
 SNOS(30,25) (single strand NQS, the  
 base in question has Phred score >= 30, the surrounding 10 bases in  
 the read have Phred  
 score >= 25), and the read must have at least 200 bp SNOS(30,25)  
 bases. Reads not uniquely  
 placed in the genome and read pairs whose two ends were not  
 consistently placed were

